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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Escherichia coli (strain O157:H7, substra col1 #text_change 09-Jul-2004 T.; K.; Ishii, K.; Yokoyama, K.; Han, C.G. T.; Hattori, M.; Shinagawa, H. crhagic Escherichia coli O157:H7 and geno coli D157:H7 and geno coli D158:H7 and geno coli D157:H7 and geno coli D157	folded gastrulatio hypothetical prote serine proteinease hypothetical prote hypothetical prote hypothetical prote glycoprotein B - a DNA topoisomerase sporozoite surface hypothetical prote lipoxygenase (EC 1 hypothetical prote masquerade precurs hypothetical prote probable metallor hypothetical prote probable metallor hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote hypothetical prote pslA protein - sli fragile x mental r hypothetical prote gene posterior requiracGAP protein - sli hypothetical prote gene posterior sex resistance protein histidine kinase h mucin 2 precursor, hemocytin - silkwohypothetical prote trithorax protein - sli hypothetical prote trithorax protein - sli hypothetical prote trithorax protein - sli hypothetical prote

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R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; A Nature 409, 529-531, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E86045
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                                                    ELLEPKGTGESKGAGESKGVGELRESNSGAENTTETQTSTSTSSLRSDPKLWLALGTVAT
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                                 ELLEPKGTGESKGAGESKGVGELRESNSGAENTTETQTSTSTSSLRSDPKLWLALGTVAT
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K.; Ag

    Apodaca,

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probable auxin-induced protein, 50455-50036 [imported] - Arabidopsis thaliana (C.Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2004 C;Accession: D86417
R.Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso Chin, C.W.; Chung, M.K.; Conm, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K. ansen, N.F.; Hughes, B.; Huizar, L.
A.Auture 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, X.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, R.; Rooney, T.; Rowley, D.; Sakano, H.
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A.;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A.;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A.;Accession: D86417
A.;Accession: D86417
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D86417
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R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.;

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu,

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein SA2097 [imported] - Staphylococcus aureus (strain N315 C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
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A; Residues: 1-166 < KUR>
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Pred. No.
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C;Superfamily: auxin-induced protein 10A
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A;Residues: 1-139 <STO>
A;Cross-references: UNIPROT:Q9C7Q5; UNIPARC:UPI00000AA867; GB:AE005172; NID:g10092232;
C;Genetics:
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A; Residues: 1-524 <WEB>
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C;Accession: S33640; S27841
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A; Accession: T31631
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C;Date: 29-Oct_1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
RESULT 7
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                                                                                                                                                                                                                                                                                                                                                      R; Webster, P.J.; Mansour,
                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Schistosoma mansoni
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                                                                                                                                                                                                                                                                                                                                                                                                                      homeotic protein smox-2, engrailed-like -
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                                                                                                                                                                            424-480/Domain:
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                                                                                                          Score 12; DB; Pred. No. 0.0
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PMID:1356008
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A; Status: preliminary
A; Status: preliminary
A; Status: preliminary
A; Marcial Status: preliminary
A; Mote: sequence extracted from NCBI backbone (NCBIN:131871, NCBIP:131872)
A; Note: sequence extracted from NCBI backbone (NCBIN:131871, NCBIP:131872)
A; Note: sequence extracted from NCBI backbone (NCBIP:131871, NCBIP:131872)
A; Note: sequence extracted from NCBI backbone (NCBIP:131871, NCBIP:131872)
A; Note: sequence extracted from NCBI backbone (NCBIP:131871, NCBIP:131872)
A; Note: sequence extracted from NCBI backbone (NCBIP:131871, NCBIP:131872)
A; Note: sequence extracted from NCBI backbone (NCBIP:131871, NCBIP:131872)
A; Note: sequence extracted from NCBI backbone (NCBIP:131871, NCBIP:131872)
A; Note: sequence extracted from NCBI backbone (NCBIP:131871, NCBIP:131872)
A; Note: sequence extracted from NCBI backbone (NCBIP:131871, NCBIP:131872)
A; Note: sequence extracted from NCBI backbone (NCBIP:131871, NCBIP:131872)
A; Note: sequence extracted from NCBI backbone (NCBIP:131871, NCBIP:131872)
A; Note: sequence extracted from NCBIP:131871, NCBIP:131871, NCBIP:131872)
A; Note: sequence extracted from NCBIP:131871, 
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S47277
                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: A36910
R;Flint, H.J.; Martin, J.; McPherson, C.A.; Daniel,
J. Bacteriol: 175, 2943-2951, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, December 1997
A;Description: The sequence of C. elegans cosmid K11D12.
A;Reference number: Z21207
A;Accession: T32661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein K11D12.1 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
                                                                                                                                                                                                                                                                                                         A;Reference number: A36910; MUID:93259938; A;Accession: A36910
                                                                                                                                                                                                                                                                                                                                               A; Title: A bifunctional enzyme, with separate xylanase and beta (1,3-1,4)-glucanase A; Reference number: A36910; MUID:93259938; PMID:8491715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   xylanase, beta(1,3-1,4)-glucanase - Ruminococcus flavefaciens C; Species: Ruminococcus flavefaciens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: S47277
A; Accession: S47277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: S47277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gp88 protein - murine cytomegalovirus
C;Species: murine cytomegalovirus, murine herpesvirus 1
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
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A;Introns: 5/3; 48/3; 90/3; 127/3; 149/3; 190/1; 207/1; 233/3;
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R; Henkhaus, J.; Wohldmann, P.; Gillam,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A36910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
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0; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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. 0.0043;
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F;541-584/Domain: Limiter F;1776-2115/Domain: III < LONG'S F;1776-115/Domain: laminin-type EGF-like homology #status / F;1776-1806/Domain: laminin-type EGF-like homology <LE2> F;1809-1856/Domain: laminin-type EGF-like homology <LE3> F;1859-1914/Domain: laminin-type EGF-like homology <LE3> F;1817-1967/Domain: laminin-type EGF-like homology <LE4>
                                                                                                                                                   A;Cross-references: FlyBase:FBgn0002526
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like h C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like homology coiled coil; disulfide bond; extracellular F;273-330/Domain: laminin-type EGF-like homology cLEG>
F;333-400/Domain: laminin-type EGF-like homology cLEG2>
F;541-584/Domain: laminin-type EGF-like homology cLEG1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Residues: 1-3712 <KUS>
A;Residues: 1-3712 <KUS>
A;Cross-references: UNIPROT:Q00174; UNIPARC:UPI000004EE1C; GB:M96388; NID:g157799; PIDN:R;Garrison, K.; MacKrell, Fessler, J.H.
J. Biol. Chem. 266, 22899-22904, 1991
A;Title: Drosophila laminin A chain sequence, interspecies comparison, and domain struct A;Reference number: S18253; MUID:92078147; PMID:1744083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Laminin A chain: expression during Drosophila development and genomic sequence A;Reference number: S28399; MUID:93049203; PMID:1425586
A;Accession: S28399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R; Kusche-Gullberg, M.; Garrison, EMBO J. 11, 4519-4527, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           laminin alpha-1 chain precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 16-Sep-1992 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
C;Accession: $28399; $18253
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C;Species: Drosophila melanogaster
C;Dsecies: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
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S12519
                                                                                                                                                                                                                                                                                                                                        A;Gene: FlyBase:LanA
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A; Residues: 1762-3712 <GAR>
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A;Residues: 1-1023 <OLS>
A;Cross-references: UNIPROT:P33438; UNIPARC:UPI000012B819; EMBL:X53286; NID:g297084;
                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPARC:UPI000016BC67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: S18253
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A;Tille: Glutactin, a novel Drosophila basement membrane-related glycoprotein with seque A;Reference number: S12519; MUID:90214632; PMID:2108864
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Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTTTTTTTTTS 404
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100.0%; Pred. No. 0.0
1ve - 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               K.; MacKrell, A.J.; Fessler, L.I.; Fessler,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>.</u>.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                     EMBL:M75882; NID:g157797; PIDN:AAA28661.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
0.0072;
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                                                                                                                    atypical <LE1>
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F;139-171/Domain:
F;172-200/Domain:
F;201-233/Domain:
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C;Superfamily: EGF homology
C;Keywords: alternative splicing; peripheral membrane protein
                                                                                                                                  F;663-695/Domain:
                                                                                                                                                                  F;597-629/Domain:
                                                                                                                                                                                                 F;531-563/Domain:
                                                                                                                                                                                                                F;498-530/Domain:
                                                                                                                                                                                                                               F;465-497/Domain:
                                                                                                                                                                                                                                                              F;399-431/Domain:
                                                                                                                                                                                                                                                                                F;366-398/Domain:
                                                                                                                                                                                                                                                                                              F;333-365/Domain:
                                                                                                                                                                                                                                                                                                                 F;300-332/Domain:
                                                                                                                                                                                                                                                                                                                            F;267-299/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Kordeli, E.; Lambert, S.; Bennett, V.
J. Biol. Chem. 270, 2352-2359, 1995
A;Title: Ankyrin-G. A new ankyrin gene with neural-specific isoforms localized at the A;Reference number: A55575; MUID:95138209; PMID:7836469
A;Accession: A55575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;2017-2061/Domain: laminin-tF;2064-2109/Domain: laminin-tF;2116-2697/Domain: I/II, hep F;2698-3712/Domain: G <DOMG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Cross-references: UNIPROT:Q12955; UNIPARC:UPI000013C497; GB:U13616; NID:g608024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Date: 03-Mar-1995 #sequence_revision 03-Mar-1995 #text_change 31-Dec-2004
C;Accession: A55575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ankyrin 3, long splice form N;Alternate names: ankyrin
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F;3529-3712/Domain: repeat G5 <RG5>
F;1847,1850,1943,2024,2196,2215,2267,2301,2323,2482,2524,2538,2569,2699,2720,2890,2938,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;2698-2863/Domain: repeat G1 <RG1>
F;2864-3048/Domain: repeat G2 <RG2>
F;3049-3223/Jomain: repeat G3 <RG3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: mRNA
A;Residues: 1-4377 <KOR>
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                                                                                                                                                                                ;564-596/Domain:
                                                                                                                                                                                                                                                ;432-464/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                            ;106-138/Domain: ankyrin repeat homology <AN02>
                                                                                                                                                                                                                                                                                                                                                                                                                             ;73-105/Domain: ankyrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Gene: GDB:ANK3
      Matches
                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross-references: GDB:424503; OMIM:600465
                                                                                                                                                                                                                                                                                                                                               234-266/Domain:
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12; Conserv
                  Similarity
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laminin-type EGF-like homology <LE7>
I/II, heptad repeats <DOM2>
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                    100.0%;
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                                 2.2%;
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homology
homology
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                                                                                                                                                                                                                                                                                                                                                                                              homology <AN03>
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                                                                             homology <AN21>
                                                                                                               homology
                Score 12;
Pred. No.
                                                                                                                             homology <AN19>
                                                                                                                                                homology
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                <AN01>
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                                                                                                                                                <AN18>
                                                                                                                                                                                                                                                                                                                                <AN07>
                                                                                                                                                                                                                                                                                                           <80NA>
                DB 2;
0.026;
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0.022;
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                                Length 4377;
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A;Note: sequence extracted from NCBI backbone (NCBIN:121249, NCBIP:121252)
C;Superfamily: Alkaline phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alkaline phosphatase (EC 3.1.3.1), intestinal type II - rat (fragment) C;Species: Rattus norvegicus (Norway rat) C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 16-Aug-2004 C;Accession: B56888
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-164 <WIL>
                                                            A; Reference number: A; Accession: T26561
                                                                                 submitted to the EMBL Data A; Reference number: Z20233
                                                                                                                                         hypothetical protein Y24F12A.d - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text C;Date: T26561
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A;Experimental source: clone Y43F8C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-108 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, October 1998 A;Reference number: Z20279 A;Accession: T26880
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A; Residues: 1-67 < ENG>
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                                                                                                                          R; Lennard, N.
                                                                                                                                                                                                                                                  RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                 #sequence_revision 15-Oct-1999 #text_change
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                                                                                                    Library,
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                                                                                                    September 1999
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0.0093;
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                                                                                                                                        A;Introns: 137/1
C;Superfamily: Caenorhabditis elegans hypothetical protein Y9D1A.2
Search completed: August 1,
                                                                                                                                                                           A;Gene: CESP:Y24F12A.d
                                                                                                                                                                                      A; Experimental source: C; Genetics:
                                                                                                                                                                                                  A;Cross-references: UNIPARC:UPI0000179900; EMBL:AL110480; PIDN:CAB54380.1; CESP:Y24F12A. A;Experimental source: clone Y24F12A
                                                                                             Matches
                                                                                                         Query Match
Best Local
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                                          112 TTTTTTTTTT
                                                                                           1 Similarity
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                                                                                                       2.0%;
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 2006, 22:38:56
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                                                                                                         Score 11;
Pred. No.
                                                                                               Mismatches
                                                                                                         DB 2;
0.013;
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                                                                                                                    Length 164;
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Job time : 50 secs

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Result
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Maximum
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Maximum Match 100%
Listing first 100
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Perfect score:
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Aay06213 BPEC E. c
Aay06220 BPEC E. c
Adc00799 Enterohae
Aeb91310 Microbial
Aee86220 Escherich
Aay06221 BHEC E. c
Abb60827 Drosophil
Aea26275 Stress to
Abp41697 Human pol
Add189021 EKMCAD pr
Aam41013 Human pol
Add289030 Antagonis
Adx07462 Cyclin-de
Abb91.64 Mouse for
Abw05424 SH3 domai
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              Aab96146 Putative Ad643142 Bacterial Abo66765 Klabsiell Adw18205 E-grandis Adc689973 Plant pol Aef21139 Candidada a Adt60207 Plant pol Aef21139 Candidomon Abm86049 Rice abio Abb674627 Pseudomon Abm86049 Rice abio Abb68251 Drosophil Abo74627 Pseudomon Adc30973 Human nov Add24466 Plant ful Adx70759 Plant ful Abb61259 Drosophil Acc81505 Nuclear r Acc81507 Mycobacte Add30240 Plant tra Abj19793 DOCK 3 tu Abj19794 DOCK 3 tu Abj19795 DOCK 3 tu Abj19795 DOCK 3 tu Abj19799 DOCK 3 tu Abj19799
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                                                                                                                                                                                                                                                                                                                                                                                          AAY06220), a novel translocated intimin receptor from an enteropathogenic Escherichia coli (EPEC) strain. The 78 kDa EPEC protein is secreted by the bacterial pathogen. Diagnosis of disease caused by pathogenic E. coli can be performed by use of antibodies that bind to Tir to detect the protein, or the use of nucleic acid probes for detection of nucleic acids encoding Tir. A kit for the detection of Tir-producing E. coli is provided. Also provided are a method of immunising a host with Tir to induce a protective immune response, and a method for screening for compounds which interfere with the binding of bacterial pathogens to their receptors
  16-AUG-1999
                                         AAY06220;
                                                                                AAY06220 standard;
                                                                                                                                                                                                                                                                                                                                                            Sequence 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Page 37; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New translocated enteropathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-337712/28.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infection; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present sequence represents the N-terminal sequence of Tir (see also
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                                                                                                                                                                                    PIGNLGNNVNGNHLIPPAPPLPSOTDGAAR
                                                                                                                                                                                                                                PIGNIGNNVNGNHLIPPAPPLPSQTDGAAR 30
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  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              intimin receptor useful for treating infection or enterohemorrhagic Escherichia coli.
                                                                                protein; 549
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                                                                                                                                                                                                                                                                                             Score 165; DB 2;
Pred. No. 1.9e-13;
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Ady07972 Plant ful
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                         (EPEC) Strain. The sequence was deduced from an isolated tir (EPEC) strain. The sequence was deduced from an isolated tir polymucleotide (see AAX5885). Tir proteins are secreted by attaching and effacing pathogens such as EPEC and EHEC (see AAX6821) E. coli. The bacterial pathogens insert their own receptors into mammalian cell surfaces, to which the pathogen then adheres to trigger additional host signaling events and actin nucleation. Diagnosis of disease caused by pathogenic E. coli can be performed by use of antibodies that bind to Tir to detect the protein or the use of nucleic acid probes for detection of nucleic acids encoding Tir polypeptide. Isolated Tir nucleic acids, Tir peptides, a recombinant method for producing recombinant Tir, antibodies which bind to Tir, and a kit for the detection of Tir-producing E. coli are provided. A method of immunising a host with Tir to induce a proteins can be used in attenuated E. coli to induce a cell-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EPEC
  ADC00799 standard; protein; 558 AA
                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents Tir, a novel translocated intimin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 55-58; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New translocated intimin receptor useful for treating infection enteropathogenic or enterohemorrhagic Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Finlay BB, Kenny B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key Location/Qualifiers Misc-difference 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tir; translocated intimin receptor; {\tt Hp90}; enteropathogenic; {\tt EPEC}; infection; diagnosis; vaccine.
                                                                                                                                                                                                                                                                                                                  pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor (formerly termed Hp90) from an enteropathogenic Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
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                                                                                                                                                                                                                                                                                                                                    mmune response to other polypeptides, e.g. antigens. A method for creening for compounds which interfere with the binding of bacter
                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "putative transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rom the DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note= "given as Xaa in the specification;
                                                                                                                                                                                                                                                                                                                receptors is further provided
                                                                                                                                                                                      100.0%; S
100.0%; S
tive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Devinney R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "putative transmembrane domain"
                                                                                                                                                                                    Score 165; DB 2;
Pred. No. 3.9e-12;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              βĄ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stein M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAA "
                                                                                                        31
                                                                                                                                                                                                                             Length 549;
                                                                                                                                                                                           Indels
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4 B X 8 X B

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of bacterial

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Gaps

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RESULT 4
AEB91310
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Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel enterohaemorragic Escherichia coli 0157:H7-specific nucleic acid molecule. A polynucleotide of the invention has anti-bacterial civity. The polypepide can be used in detection and/or treatment of 0157:H7 infection. The nucleotide sequence of the genome of Enterohaemorragic E coli 0157:H7 was determined. The present sequence represents an E. coli 0157:H7-specific polypeptide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterohemorragic Escherichia coli O157:H7-specific nucleic acid molecule and a polypeptide and its use, a polypeptide, a vector and a host cell.
                                                                                                                                          antiinflammatory; respiratory-gen.;
gastrointestinal-gen.; urinary tract
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli; 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                enterohaemorragic; anti-bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterohaemorragic E. coli 0157:H7-specific protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-DEC-2003
           06-FEB-2004; 2004IN-DE000173.
20-JUL-2004; 2004US-0589227P.
                                                                                                                     Escherichia coli
                                                                                                                                                                              algorithm; adhesin; pharmaceutical; vaccine; drug screening;
                                                                                                                                                                                                       Microbial
                                                                                                                                                                                                                                                                               AEB91310 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-451640/43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADC00799
                                             07-FEB-2005; 2005WO-IN000037.
                                                                                             WO2005076010-A2
                                                                                                                                                                                                                                20-OCT-2005
                                                                                                                                                                                                                                                       AEB91310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-JAN-2001; 2001JP-00112010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-JAN-2002; 2002JP-00015959
                                                                      18-AUG-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYTS-)
                                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                          N
                                                                                                                                                                                                                                                                                                                                                               1 PIGNLGNNVNGNHLIPPAPPLPSQTDGA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNIV TSUKUBA.
                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID
                                                                                                                                                                                                                                                                                                                                         PIGNLGHNPNVNNSIPPAPPLPSQTDGA 29
                                                                                                                                                                                                       pathogen
                                                                                                                                                                   pertussis infection; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NO 844; 2067pp; Japanese.
                                                                                                                                                                                                                                                                             protein; 558
                                                                                                                                                                                                      adhesin protein sequence,
                                                                                                                                                                                                                                                                                                                                                                                                    74.5%;
82.1%;
                                                                                                                                                                                                                                                                                                                                                                                          2
                                                                                                                                                                                                                                                                                                                                                                                                    Score 123; DB 7;
Pred. No. 7.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                               ₹
                                                                                                                                                      gastric ulcer; antiulcer;
                                                                                                                                            infection; antimicrobial; uropathic.
                                                                                                                                                                                                       SEQ ID
                                                                                                                                                                   pneumonia
                                                                                                                                                                                                                                                                                                                                                                                                              Length 558
                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                        NO:20
                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          844.
                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Query Match

Local

Similarity

74.5%; 82.1%;

Score 123; DB 9; Pred. No. 7.3e-07;

Length 558;

0

Sequence 558

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CC each of the computed five attributes, and identifying the adhesin and CC adhesin-like proteins having probability of being an adhesin (Pad) as CC equal or greater than 0.51. Also claimed is a set of 274 annotated genes cC encoding adhesin and adhesin-like proteins, having 274 fully defined 162-CC 11151 base pair (SEQ ID NO: 385-658) sequences; a set of 105 hypothetical CC genes encoding adhesin and adhesin-like proteins, having 174 fully defined 162-CC 11151 base pairs (SEQ ID NO: 385-658) sequences; a set of 105 hypothetical CC genes encoding adhesin-like proteins, having 274 fully defined 53-3716 base CC pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-like proteins, having 105 fully defined 53-3716 base CC pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-like proteins, having 105 fully defined 106-5291 base pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-like CC patroteins, having 105 fully defined 106-5291 base pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin-like CC proteins, of therapeutic potential, and identifying adhesin-like CC proteins, of therapeutic potential, and identifying and short-listing CC useful for identifying putative adhesins that are important in drug CC discovery and preventing therapeutics for whooping cough, pneumonia, CC distantly related organisms, and from bacteria belonging to a wide CC distantly related organisms, and from bacteria belonging to a wide conjugue proteins. The present sequence is a microbial pathogen adhesin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          identifying adhesin and adhesin-like proteins, by computing the sequence-based attributes of protein sequences using five attribute modules of a neural network software, training an artificial neural network (ANN) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computational method for identifying adhesin and adhesin like molecules, comprises computing sequence-based attributes of protein sequences using neural network software and training an artificial neural network.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sachdeva G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to a computational method (M1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (COUL ) COUNCIL SCI &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; SEQ ID NO 20; 402pp; English.
                                                    sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kumar K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IND RES SOUTH AFRICA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jain P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brahmachari SK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ramachandran
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RESULT 5
AEE86220
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Matches
                                                                                                        Diagnosis; therapeutic; screening; escherichia coli infection;
         20-MAY-2004; 2004US-0573600P
                                                                               Escherichia coli
                                                                                                                          Escherichia coli translocated intimin receptor (Tir) protein.
                                                                                                                                                               AEE86220;
                                                                                                                                                                                AEE86220 standard;
                          20-MAY-2005; 2005US-00134563
                                            29-DEC-2005
                                                             US2005287569-A1
                                                                                                                                                                                                                                     1 PIGNLGNNVNGNHLIPPAPPLPSQTDGA 28
                                                                                                                                                                                                                                                                23
                                                                                                                                                                                                                             N
                                                                                                                                                                                                                             PIGNIGHNPNVNNSIPPAPPLPSQTDGA 29
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                            (first
                                                                                                infection;
                                                                                                                                                                               protein;
                                                                                                                                            entry)
                                                                                                 translocated intimin
                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                0,
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RESULT 6
AAY06221
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         corresponding polynuclectides. The EspFU polypeptides are EspF-like
polypeptides encoded by genes of the cryptic prophage CP-933U of
enterohemorrhagic Escherichia coli (EHEC) or enteropathogenic Escherichia
Coli (EPEC) that binds to a neuronal wiskott-aldrich syndrome protein (N-
WASP) polypeptide or restores the actin pedestal formation activity of
enteropathogenic E. coli (EPEC) strain KC12. The invention further
crelates to a method of identifying a candidate compounds capable of
binding to and/or modulating the activity of EspFU and EspFU-interacting
to and/or modulating the activity of EspFU and EspFU-interacting
crinibits protein-protein interactions between EspFU and EspFU-interacting
proteins such as N-WASP, transducer of Cdc42-dependent actin assembly-1
(Toca-1) and p21-activated kinase 1 (Pakl). EspFU polynucleotides are
useful for treating EHEC infection. The present sequence is the
enterohemorrhagic Escherichia coli translocated intimin receptor (Tir)
protein. This sequence is critical for the formation of actin pedestals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                           10-NOV-1998;
                                                                                                          20-MAY-1999.
                                                                                                                                       WO9924576-A1
                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                  Escherichia coli
                                                                                                                                                                                                                                                                                         Tir; translocated intimin receptor; Hp90; enterohaemorrhagic; EHEC;
                                                                                                                                                                                                                                                                                                                           EHEC E.
                                                                                                                                                                                                                                                                                                                                                         16-AUG-1999
                                                                                                                                                                                                                                                                                                                                                                                      AAY06221;
                                                                                                                                                                                                                                                                                                                                                                                                                     AAY06221 standard; protein; 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel EspFU polypeptides and their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 12; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel purified polypeptide having six residues of EspF-U, and binding neuronal Wiskott-Aldrich syndrome protein polypeptide, useful for identifying EspF-U activity modulating compound.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2006-065745/07.
                (UYBR-) UNIV BRITISH COLUMBIA
                                              12-NOV-1997;
                                                                                                                                                                                                                                                                              infection; diagnosis; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CAMP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LEON/) LEONG J M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ч
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                                                                                                                                                                                                                                                                                                                       coli translocated intimin receptor (Tir).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIGNLGNNVNGNHLIPPAPPLPSQTDGA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIGNLGHNPNVNNSIPPAPPLPSQTDGA 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Campellone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                             97US-0065130P.
                                                                         98WO-CA001042
                                                                                                                                                                                                       453
                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                    causing
                                                                                                                                                                  /note= "encoded by codon of 1 apparent nucleotide, causing frameshift in the DNA sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.5%;
82.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 123; DB 10;
Pred. No. 7.3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 558;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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RESULT 7
ABB60827
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            signaling events and actin nucleation. Diagnosis of disease caused by pathogenic E. coli can be performed by use of antibodies that bind to Tir to detect the protein or the use of nucleic acid probes for detection of nucleic acids encoding Tir polypeptide. Isolated Tir nucleic acids, Tir peptides, a recombinant method for producing recombinant Tir, antibodies which bind to Tir, and a kit for the detection of Tir-producing E. coli are provided. A method of immunising a host with Tir to induce a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents Tir, a novel translocated intimin receptor (formerly termed Hp90) from an enterohaemorrhagic Escherichia coli (EHEC) strain. The sequence was deduced from an isolated tir polymucleotide (see AAX58859). Tir proteins are secreted by attaching a effacing pathogens such as EHEC and EPEC (see AAY06220) E. coli. The bacterial pathogens insert their own receptors into mammalian cell surfaces, to which the pathogen then adheres to trigger additional host surfaces, to which the pathogen then adheres to trigger additional host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protective immune response is also provided. In addition, Tir fusion proteins can be used in attenuated E. coli to induce a cell-mediated immune response to other polypeptides, e.g. antigens. A method for screening for compounds which interfere with the binding of bacterial
                                               WPI; 2001-656860/75
                                                                                                                                           23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                           23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                                                                                                                           Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                        26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB60827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pathogens to their receptors is further provided
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Page 55-58; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New translocated intimin receptor useful for treating infection by enteropathogenic or enterohemorrhagic Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAX58859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-337712/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Finlay BB,
                              N-PSDB; ABL04930.
                                                                                                                                                                                                                            27-SEP-2001.
                                                                                                                                                                                                                                                           WO200171042-A2
                                                                                                                                                                                                                                                                                                                           pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster polypeptide SEQ ID NO 9273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABB60827 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enteropathogenic or
                                                                                                             (PEKE ) PE
                                                                               JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 PIGNLGNNVNGNHLIPPAPPLPSQTDGA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  559 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIGNIGHNPNVNNSIPPAPPLPSQTDGA 29
                                                                                                               CORP NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kenny B,
                                                                             Adams M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                           2000US-0191637P
2000US-00614150
                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74.5%;
82.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Devinney R,
                                                                               닭
                                                                               PWD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 123; DB z; Pred. No. 7.3e-07;
                                                                               Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stein
                                                                               띹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 559;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              by attaching and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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New isolated nucleic acid detection reagent for detecting 1000 or more

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RESULT 8
AEA26275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
polypeptides, the DNA sequences which encode them and their use in creating transgenic plants. The transgenic plant and methods are use for producing commercially or agriculturally useful plants having improved tolerance to drought, shade and low nitrogen conditions when
                                                                                   Example 8; SEQ
                                                                                                                      New transgenic plants plants having improved
                                                                                                                                                                           WPI;
                                                                                                                                                                                                              Repetti P,
Sherman BK,
                                                                                                                                                                                                                                                                                       13-NOV-2003; 2003US-00714887
05-DEC-2003; 2003US-0527658P
05-FEB-2004; 2004US-0542928P
                                                                                                                                                                                                                                                                                                                                                                                                                        Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                transcription factor; stress tolerance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stress tolerant plant-related transcription factor protein SeqID116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEA26275 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                      26-MAY-2005
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                                                                                                                                                                                                                                                                                                                                           12-NOV-2004; 2004WO-US037584
                                                                                                                                                                                                                                                                (MEND-) MENDEL BIOTECHNOLOGY INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               interactions
                                                                                                                                                                          2005-372386/38
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Kumimoto RW,
C, Morrison TA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                         improved
                                                                                 ID NO 116; 407pp; English
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                                                                                                                       for producing d tolerance to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         transgenic plant; agriculture; drought resistance;
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                                                                                                                                                                                                  Libby
                                                                                                                                                                                                          Creelman RA, Ratcl
Gutterson NI, Reub
Keddie JS, Jiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for elucidating cell signaling and cell-cell
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Pred. No.
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                                                                                                                      commercially or agriculturally useful drought, shade and low nitrogen
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                                                                                                                                                                                                           Ratcliffe OJ, Canal
Reuber TL, Pineda
Jiang C, Century KS,
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                                 are useful
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RESULT 9
ABP41697
ID P41697
ID P41697
AC ABP4

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Best Local (
The invention relates to 2175 novel human ovarian antigens (ABP41054-ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also encompasses polypeptides 90% identical and polymucleotides 95% identical to the sequences of the invention. The invention additionally relates to recombinant vectors and host cells comprising human ovarian antigen polymucleotides, antibodies against human ovarian antigens, and the use of ovarian antigen polymucleotides and polypeptides in diagnosing, treating, prognosing or preventing various ovary and/or breast-related disorders. Such conditions include ovarian cancer and breast cancer, and metastacic tumours of ovarian or breast origin, reproductive system disorders (e.g., infertility, disorders of pregnancy, anovulation, polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       useful in cancer),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour; ovarian cancer; breast cancer; tumour; reproductive system disorder; infertility; pregnancy disorder; anovulation; polycystic ovary syndror PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection; inflammatory condition; immune disorder; blood disorder; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disorder; respiratory disorder; drug screening; gene therapy; chromosome mapping; forensic analysis; antibody preparation; cytostatic; immunomodulatory; neuroprotective; antiinflammatory; gynaecological; reproductive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecules encoding novel ovarian polypeptides, useful in the prevention, treatment and diagnosis of cancer (e.g. overancer), immune disorders, cardiovascular disorders and neurological
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        compared to wild-type reference plants. The plant transcription factor protein which was of the transgenic plants of the invention.
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DB; ABQ54774.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                2829;
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Pred.
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RESULT 10
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AC AAM39
XX AAM3 PAT 22-OC
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21-JAN-2000;
25-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and vaginitis), immune disorders (e.g., congenited and acquired immunedeficiencies, autoimmune oophoritis, systemic lupus erythematosus), blood-related disorders (e.g., anaemia), cardiovascular disorders, blood-related disorders, neurological disorders, gastrointestinal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peripheral nervous system; neuropathy; central nervous system; CNS; Alzhelmer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; BNy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                         WPI; 2001-442253/47.
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                                                                                                                                              P. J. Ž.
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Wang Z,
Goodrich
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2000US-0048725.
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2000US-00662191.
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immunosuppressant; cytostatic; gene therapy; s system; neuropathy; central nervous system;
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44.4%;
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Pred. No. 98;
5; Mismatches
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Yang Y,
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Novel nucleic acids and polypeptides, useful for treating disorders such

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(Gaucher's disease; myotonic dystrophy; sickle cell anemia; thalassemia;

KW Wilms' tumor; immunological disorder; acquired immunodeficiency syndrome;

KW AIDS; adult respiratory distress syndrome; allergy; anemia; asthma;

KW Goodpasture's syndrome; gout; Grave's disease; multiple sclerosis;

KW Goodpasture's syndrome; gout; Grave's disease; multiple sclerosis;

KW steoporosis; psoriasis; rheumatoid arthritis; scleroderma;

KW systemic lupus erythematosus; ulcerative colitis; uveitis;

KW meurological disorder; epilepsy; stroke, Alzheimer's disease;

KW meningicn's disease; parkinson's disease; multiple sclerosis;

KW meningitis; periodic paralysis; mental disorder; mood; anxiety;

KW schizophrenia; amnesia; diabetic neuropathy; connective tissue disorder;

KW osteoporosis; paget's disease; osteonecrosis; osteomyelitis;

KW chondrosarcoma; giant cell tumor; psoriatic arthritis;

KW actinic keratosis, atherosclerosis; hepatitis; psoriasis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, Chemotactic/Chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antianemic; antiasthmatic; immunosuppressive; antiatherosclerotic; dermatological; nephrotrophic; antigout; antithyroid; neuroprotective; osteopathic; antipsoriatic; antirheumatic; antiarthritic; antiulcer; antiinflammatory; ophthalmological; anticonvulsant; antiparkinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nootropic; antisickling; antianemic; antitumor; anti-HIV; antiallergic; antianemic; antiasthmatic; immunosuppressive; antiatherosclerotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cytostatic; hepatotrophic; gene therapy;
human extracellular matrix and cell adhesion molecule; ECMCAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibacterial; virucide; tranquilizer; neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECMCAD protein 5773251CD1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 4; SEQ ID NO 2372; 10078pp; English
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12; Conser
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Pred. No. 1.6e+02;
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antidiabetic;
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c fibrosis;
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This sequence represents one of the novel proteins.
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Best Local (
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18-JUL-2000;
12-OCT-2000;
12-OCT-2000;
27-OCT-2000;
14-NOV-2000;
22-OCT-2001
                                AAM41013;
                                                                AAM41013
                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated human extracellular matrix and cell adhesion molecules useful for treating, preventing connective tissue disorder e.g. useful for treating, preventing connective tissue disorder e.g. cystic fibrosis,
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Lu DAM,
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                                                                                                                                                                                                                                     Local Similarity
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DB; ADI28057.
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, Marcus GA, Zingler KA, Gandhi AR, Lal P. Kearney
Yao MG, Walia NK, Elliot VS. Patterson C. Khan FA;
Hafalia AJA, Policky JL, Au-Young J. Lu Y. Borowsk
amkumar J. Yang J. Gururajan R. Warren BA, Gietzen K
lick DA, Lee EA, Thangavelu K, Delegeane AM, Lee S;
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2000US-0240111P.
2000US-0244021P.
2000US-0248887P.
2000US-0249570P.
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(first entry)
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                                                                protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   o a novel isolated human extracellular matrix and (referred to as ECMCAD 1-36), its biologically
                                                                                                                                                                                                                    Score 58.5; D
Pred. No. 1.6e
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RESULT 13
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ADQ89830 standard; protein;

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Query Match
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                                                                                                                                                                          immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral nervous hazheiner's, Parkinson's disease, Huntington's disease, such as Alzheiner's, Parkinson's disease, Huntington's disease, such as Alzheiner's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activitys such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and c.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
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Wang
                                                                                                                                      Sequence 1086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human nucleic acids (AAI57798-AAI61369) and encoded polypeptides (AAM38642-AAM42213) with nootropic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-DEC-1999; 99US-00471275.
21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-UUN-2000; 2000US-00598042.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example
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03-AUG-2000;
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Wang Z, Weh
Goodrich R,
IGNLGNNVNGNHLIPPAPPLPSQTDGA 28
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2000US-00653450.
2000US-00662191.
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2000US-00727344
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Wehrman T,
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                                          Score 58.5; DB 4;
Pred. No. 1.8e+02;
5; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen R,
Xu C,
RT;
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Xue
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Yang Y,
                                                                                       Length 1086;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ren F, W
Zhang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         haemostatic;
                                            ű,
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I, Zhao (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CNS
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                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a polynucleotide for preventing, treating or diagnosing a disease in an individual. The composition or the polypeptide, polynucleotide or RNA precursor, or antibody is useful for diagnosing, preventing or treating diseases (e.g. cell proliferative diseases such as cancer) in an individual. These may also be used for identifying substances capable of binding to or modulating the function of the polypeptide, capable of affecting the function of the corresponding gene, or capable of inhibiting the cell division cycle or cell cycle progression, preferably mitosis and/or meiosis. The present sequence represents an antagonist of cell cycle progression protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New cell cycle progression genes and proteins for modulating cell cycle progression in cells, for preventing, treating or diagnosing cell proliferative diseases (e.g. cancer) or for identifying modulators of
                WO2005012875-A2
                                         Homo sapiens
                                                                  cytostatic;
                                                                                            Cyclin-dependent kinase modulation biomarker SEQ ID NO
                                                                                                                       21-APR-2005
                                                                                                                                                  ADX07462;
                                                                                                                                                                           ADX07462 standard; protein; 2602 AA
                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; SEQ ID NO 260; 461pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glover D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-JAN-2003;
06-MAY-2003;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-DEC-2003; 2003WO-GB005635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; cancer; cell division cycle; mitosis; meiosis; cell cycle progression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antagonist of cell cycle progression polypeptide #130.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-OCT-2004
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                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                             2411 VGGMPFSVYGNAMİPPVAPIP---DGA 2434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2004-544089/52.
)B; ADQ89829.
                                                                                                                                                                                                                                                                       N
                                                                                                                                                                                                                                                                                               l Similarity
12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or meiosis.
                                                                                                                                                                                                                                                                      IGNLGNNVNGNHLIPPAPPLPSQTDGA 28
                                                                                                                                                                                                                                                                                                                                                     2486 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bell G,
                                                                  cyclin-dependent
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2003US-0439123P
2003US-0468402P
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                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                             35.5%;
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                                                                                                                                                                                                                                                                                               Score 58.5; DB 8;
Pred. No. 4.3e+02;
5; Mismatches 7
                                                                    kinase; cdk; biomarker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Midgley
                                                                                                                                                                                                                                                                                                                           DB 8;
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CC whether a mammal will respond or is responding to an anti-cancer agent to that modulates cyclin-dependent kinase (cdk) activity. The method CC comprises measuring the level of one or more biomarkers selected from CC 2774 biomarkers given in the specification (nucleotide sequence SEQ ID CC NO:1246 (Genbank EST W28729) is especially preferred). The method of the CC invention is utilized in a kit for determining or predicting whether CC microarray comprising the invention also describes a method for CC utilizing individualized genetic profiles for treatment by an agent CC utilizing individualized genetic profiles for treating diseases and CC disorders based on patient's response and molecular level, specialized CC against the biomarkers and a cell culture model to identify biomarkers. CC The cdk modulator is preferably N-5-[[5-(1,1-Dimethylethyl)-2-CC oxazolyl]methyl]thio]-2-thiazolyl-4-piperidine carboxamide, 0.5-L-CC tartaric acid salt. Note: The sequence data for this patent did not form CC cart of the printed specification, but was obtained in electronic format CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. This CC sequence represents a biomarker used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Biomarkers useful for predicting to a cancer treatment comprising dependent kinase activity.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                This invention describes a novel method of predicting or determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Li M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-2004; 2004WO-US024424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BRIM ) BRISTOL-MYERS SQUIBB CO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2005-163068/17.
DB; ADX07461.
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  2602 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2027; 141pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  or determining administration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the response of a mammal of a modulator of cyclin-
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Best Local (
 2527 VGGMPFSVYGNAMÍPPVAPIP---DGA 2550
                    N
                                       l Similarity
12; Conserv
                   IGNLGNNVNGNHLIPPAPPLPSQTDGA 28
                                        Conservative
                                                 35.5%;
                                       5.
                                                 Score 58.5; DB 9;
Pred. No. 4.5e+02;
                                       Mismatches
                                                          9
                                                          Length 2602;
                                         Indels
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RESULT 16
ABB99164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 10
                                                                                                                                              Mouse; formin-2; recurrent pregnancy loss; formin-2; Fmn-2; RPL;
12-APR-2001; 2001US-00835232
                                                                                                     qa apM
                                                                                                                                     spontaneous
                                                                                                                                                                                          Mouse formin-2.
                                                                                                                                                                                                                          22-NOV-2002
                                                                                                                                                                                                                                                            ABB99164;
                                                                                                                                                                                                                                                                                             ABB99164 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 809
                                  25-JUL-2002
                                                                  US2002098489-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this patent specification but is based on sequence the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to constructing (cells in which both alleles of a gene a one allele by insertion or replacement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Constructing strains for identifying gene products as effective targets for therapeutic intervention, by inactivating in the strain one allele of a gene and placing other allele of the gene under conditional expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20-FEB-2001; 2001US-00792024.
22-AUG-2001; 2001US-0314050P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 44; SEQ ID NO 7691; 167pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002-566694/60.
                                                                                                                                                                                                                                                                                                                                                                                    17
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                                                                                                                                   abortion;
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                                                                                                                                                                                                                                                                                             protein; 1567 AA
                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.2%;
47.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Boone
                                                                                                                                     miscarriage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 58; DB 5;
Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (M1) a strain of diploid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohlsen
                                                                                                                                                                                                                                                                                                                                                                                                                                                 7;
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RESULT 17
ABW01569
ID ABW01569
ID ABW01
XX ABW01
XX ABW01
XX Recux
KW Recux
KW mouse
XX Mus m
PN US200
XX 11-SE
PF 03-DE
XX 13-AE
PR 12-AE
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Best Local S
Matches 11
                        Diagnosing recurrent pregnancy loss comprises examining formin-2 a mutation and measuring biological activity and expression of fidentified to play a role in occyte development.
                                                                                                                                  N-PSDB; AAD62829.
                                                                                                                                                                                                                                                                    (LEDE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel method for determining whether a patient has an increased risk for recurrent pregnancy loss, involving determining whether the formin-2 (Fun-2) gene of the patient has a mutation. The method of the invention is useful for determining whether a patient has a increased risk for recurrent pregnancy loss (RPL/recurrent spontaneous abortion/miscarriage). The sequence represents the murine formin-2 protein of the invention
                                                                                                                                                                                                                                                                                                                                               13-APR-2000; 2000US-0196811P
12-APR-2001; 2001US-00835232
                                                                                                                                                                                                                                                                                                                                                                                                                               03-DEC-2002; 2002US-00308485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2003170683-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse formin (Fmn)-2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining whether patient has increased risk for recurrent loss by determining whether formin-2 (Fmn-2) gene of patient mutation, or by measuring Fmn-2 biological activity or Fmn-2
                                                                                                                                                             WPI; 2003-830607/77
                                                                                                                                                                                                            Leder P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recurrent pregnancy loss; RPL; formin-2; Fmn-2; diagnosis; therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABW01569;
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LEADER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 NLGNNVNGNHLIPPAPPLP 22
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LEADER B.
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Pred.
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                                               1-2 gene for formin-2
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RESULT 18
ABB580090
ID ABB580900
AC ABB580090
AC ABB580
AC ABB580090
AC ABB580
AC AB580
AC AB5
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                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL1616-ABL30511), expressed DNA sequences (ABL01610-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of diagnosing recurrent pregnancy loss (RPL). The method involves examining formin (Fmn)-2 gene for a mutation and measuring biological activity and expression of Fmn-2, in which decreased levels indicates an increased risk for RPL; or examining the person's formin-2 gene for polymorphisms, in which the presence of a polymorphism indicates an altered risk for RPL. The method is used for diagnosing and treating RPL e.g. in humans. The present sequence is mouse
   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 1062; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
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11-JUL-2000; 2000US-00614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Drosophila melanogaster polypeptide SEQ ID NO 1062.
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Pred. No.
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3e+02;
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Query Match

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RESULT 19
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Matches
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                                          containing functional domains containing functional domain. The new method sequence to, the original target function to be identified. enables proteins having a common function to be identified. Identification of novel SH3 proteins will be useful for a better understanding of cell growth, malignancy, signal transduction processes, etc. New candidate drugs can be identified, and their specificities (e.g. etc. New candidate drugs can be assessed using the method of the
                                                                                                                                                   recognition units. These sequences were used as parts of multivalent recognition unit complexes used in the method of the invention. The method of the invention is for identifying polypeptides containing functional domains of interest (especially SH3 domains). It comprises contacting a multivalent recognition unit (RU) complex with a number of peptides and identifying polypeptides having a selective binding affinity for the RU complex. The method is based on functional similarities and does not rely on sequence similarities. Prior methods only gave limited success for identifying proteins containing an SH3 domain due to the minimal sequence homology among known SH3 proteins. Multivalent RU complexes are particularly suited to screening for polypeptides containing functional domains that are similar to, but not identical in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CYTO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Src-homology region 3 domain; human; mouse; SH3 domain; cell growth; cellular signalling element; cellular structural element; malignancy; protein identification; functional domain; protein screening; cellular signal transduction process; binding peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying polypeptide(s) having specific functional domain (esp.
domain) - comprises detecting selective binding to recognition uni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                          AAW05421-W05424 represent Src-homology region 3 (SH3)
                                                                                                                                                                                                                                                                                                                                                                                                             Example;
                                                                                                                                                                                                                                                                                                                                                                                                                                            regardless of sequence homology.
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UNIV NORTH CA
                                                                                                                                                                                                                                                                                                                                                                                                           Page 87; 174pp; English.
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96US-00630915.
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RESULT 20
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Best Local Similarity
Matches 11; Conserv
        sequences can be used in gene therapy. ORFX sequences, cirrhosis of liver, provided the provided the provided between the content of the content 
                                                                                                                                                                                                                                                                                                                                          treating or preventing a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating syndrome associated with ORFX-associated disorder. ORFX polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 16292; 1037pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000; 2000US-0206132P
29-AUG-2000; 2000US-0228716P
                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes substantially purified human proteins (referred to as open reading frame, ORFX, where X is 1-11491 (see Table in the specification). ABN15762 to ABN27252 encode the human ORFX proteins given in ABP00010 to ABP11500. ORFX proteins are useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ABN23907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human ORFX protein sequence SEQ ID NO:16292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease;
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Pred. No. 5.5;
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disease, and f
lung or liver
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                                                                                                          herpesvirus isolate, for example Equine herpesvirus type 1 (EHV-1) or type 4 (EHV-4), which comprises using a genetic marker, especially an ORF30-ml region marker. The invention may be useful for the production of compounds with a virucide activity or for the development of a vaccine. The method, kit and sequence of the EHV-1 strain V592 polymerase ORF30-ml region are useful for assessing the virulence of a herpesvirus or neurovirulence. The vaccine is useful for immunising a host against a herpesvirus disease and for treating disease. The present sequence is that of a peptide which is related to the invention.
                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           virulence; herpesvirus; Equine herpesvirus type 1; EHV-1; EHV-4; Equine herpesvirus type 4; genetic marker; ORF30-ml region marke virucide; vaccine; EHV-1 strain V592 polymerase ORF30-ml region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reperfusion injury in various tissues and conditions resulting from systemic cytokine damage. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                    Disclosure; Page 43; 63pp; English.
                                                                                                                                                                                                                                                                                                 to an ORF30-ml region.
                                                                                                                                                                                                                                                                                                             Assessing the virulence of a he treating herpesvirus infection,
                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-143877/14.
                                                                                                                                                                                                                                         This invention relates to a novel method of assessing the virulence of
                                                                                                                                                                                                                                                                                                                                                                                   Davis Poynter N, Nugent J,
                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUL-2002; 2002US-0398576P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Equine herpesvirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Equine herpesvirus type 1-related peptide #1.
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                                                                                                                                                                                                                                                                                                                                                                                                                (ANIM-) ANIMAL HEALTH TRUST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurovirulence; herpesvirus disease.
                                           Local Similarity
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                              Conservative
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Pred. No. 36;
1; Mismatches
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on, by using
                                           Score 56;
Pred. No.
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                             Mismatches
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13;
                                                                                                                                                                                                                                                                                                              isolate, useful in preventing or virulence marker corresponding
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RESULT 22
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                                                                                                                                                                                                                                                                                                 Eucalyptus grandis or Pinus radiata. The present sequence is one such transcription factor. The transcription factor may be used to produce a plant having modified gene expression such as a woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or mahogany species or to modify the activity of a polypeptide in a plant. The transcription factors of the present invention are members from the following families of regulatory proteins: bZIP, bZIP family of G-box binding factors, basic helix-loop-helix zipper, homeotic/homeodomain/homeobox/MADS, homeodomain aripper, LIM domain, AP2 and EREBS, zinc finger domains of type 2
                                                                                                                                                                                                                                                                                                                                                                                                                                    The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (GENE-)
 06-AUG-2003
11-SEP-2001
                                            AAG84951;
                                                                       AAG84951 standard;
                                                                                                                                                                                                                                                             Sequence 145 AA;
                                                                                                                                                                                                                                                                                      Cys2His2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8; Page 284-285; 747pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide encoding a plant transcription factor for producing a plant e.g. a woody plant, preferably eucalyptus or pine, having modified gene expression or modified activity of a polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-579369/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wood M,
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18-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           homeodomain zipper; LIM domain; AP2; ERI
type 2 Cys2His2; CCAAT box element; MYB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant; transcription factor; gene expression; eucalyptus; pine; acacia; poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor; basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS; homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eucalyptus grandis transcription factor protein sequence #203
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                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                  present invention relates to novel plant transcription factors from
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                                                                                                                                                                                                    l Similarity
10; Conserv
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                                                                                                                                            GGVGDNNNGGYLHSPLSVMPLKSDGS 86
                                                                                                                                                                        GNLGNNVNGNHLIPPAPPLPSQTDGA 28
                                                                                                                                                                                                                                                                                      CCAAT box elements and MYB
                                                                                                                                                                                                    Conservative
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(revised)
(first entry)
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99US-0149485P.
                                                                      protein;
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38.5%;
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Pred. No.
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RESULT 24
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                                                                                                                                                                                                                                                                                                                                                                                    The invention provides the primary nucleotide sequence of the WSBV genome (AAH62889), predicted transcript sequences (AAH62889) and encoded proteins (AAG84910-AAG85051) and oligonucleotide sequences (AAH62840-63160) suitable for use as primers or probes. The nucleic acid molecules and proteins of the invention are useful for diagnosis and monitoring viral infection, in screens for antiviral agents and for monitoring viral gene expression or activity during a treatment regimen. The nucleic acid molecules are also useful as antisense constructs to control viral gene expression in infected cells and tissues and to create
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Primary nucleotide sequence of the shrimp white spot Bacilliform virus (WSBV), useful for producing viral polypeptides that can be used to screen for agents that are useful for treating WSBV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shrimp white spot Bacilliform virus; antiviral agent; gene expression; ant transgenic viral resistant shrimp.
                                                                                                                                29-OCT-2001
                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                               transgenic field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Fig 3; 626pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        White spot syndrome virus.
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                                                         Pyrococcus abyssi.
                                                                                Hyperthermophilic archaeon; hyperthermophilic protein
                                                                                                        Putative P. abyssi 5-enolpyruvylshikimate-3-phosphate synthase.
                                                                                                                                                                              AAB96146 standard; protein; 410
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THIRD INST OCEANOGRAPHY
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27-OCT-2000

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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant DNA construct; transformed plant; improved plant; cold tolerance; heat tolerance; drought tolerance; herbicide; pathogen tolerance; pest tolerance; plant disease resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to the genomic sequence of Pyrococcus abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such P. abyssi protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110 degrees centigrade. Note: This patent is in the same patent family w0200065062, which contains additional sequences as shown in AAB99132-AAB99143, AAH75903-AAH75920 and AAG66436
                                                                                                                                                                                                                                                                                                                                                                                      Bacteria.
    Cao Y,
                                                                          (SLAT/)
(CHEN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        bacterial
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                                                                                                                                                                                           21-FEB-2002; 2002US-0360039P
                                                                                                                                                                                                                                          20-FEB-2003; 2003US-00369493
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Querellou J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 7; Page 783-784; 1657pp; French.
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                                                                     HINKLE
SLATER
CHEN X.
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  Hinkle GJ,
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                                                 GOLDMAN B
                                                                                                                                                CAO Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   phosphorus; photosynthesis; lignin;
polypeptide.
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    Slater
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Pred. No. 1.3e+02;
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  Chen
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W, Heilig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pyrococcus abyssi encode proteins
  Goldman BS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          galactomannan;
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The invention relates to a recombinant DNA construct comprising a CC promoter functional in a plant cell, where the promoter is positioned to CC provide for expression of a polynucleotide encoding a polypeptide from a CC microbial source. The invention also relates to a transformed plant CC comprising the recombinant DNA construct and a method of producing a CC transformed plant by a crop plant and construct and a method of producing a crop plant CC such as maize or soybean. The method of producing a transformed plant CC such as maize or soybean. The method of producing a transformed plant cCC inventor of the construct and growing the transformed plant with the CC recombinant DNA construct and growing the transformed plant with the CC improved plant properties. CC improved plant properties, e.g. improved cold, heat or drought tolerance, CC improved plant properties, e.g. improved cold, heat or drought tolerance, CC improved plant properties, e.g. improved cold, heat or drought tolerance, CC increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of CC content, improved yield by modification of carbohydrate, nitrogen or CC phosphorus use and/or uptake, by modification of photosynthesis or by condition, improved plant growth and development under at least one stress condition, improved lignin production or improved galactomanan CC condition, improved lignin production or improved galactomanan CC condition. Note: The sequence data for this patent did not CC form part of the printed specification but was obtained in electronic CC format from USPTO at sequence data for this patent did not compared the printed specification but was obtained in electronic CC format from USPTO at sequence data for this patent did not compared the printed specification but was obtained in electronic CC format from USPTO at sequence data for this patent did not format from USPTO at sequence data for this patent did not format from the printed specifi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for expression of a polynucleotide encoding a polypeptide from a microbial source, useful for producing plants with improved properties.
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RESULT 26
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Best Local (
                                                                                                            Recombinant
                                                                                                                         Klebsiella
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                                                                                                                                                               ABO66765 standard;
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                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                            IGNLGNNVNGNHLI PPAPPLPSQTD
                                                                                                                        pneumoniae polypeptide seqid 13282
                                                                                                     expression vector; transcription regulatory element; pneumoniae protein; antibacterial; Vaccine.
                                                                                                                                                                                                                         Conservative
                                                                                                                                     (first entry)
                                                                                                                                                              protein;
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WPI; 2003-895346/82

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Osborne

GENOME

29-JAN-1999;

99US-0117747P THERAPEUTICS CORP

27-JAN-2000; 2000US-00489039

US6610836-B1

Klebsiella pneumoniae.

Klebsiella

pneumoniae protein;

밁 8

Sequence 410

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RESULT 27
ADW18205
ID ADW18205
AC ADW18
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Forster RLS,
Phillips J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes a new isolated nucleic acid encoding a Klebsiella pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a
                                    DNA in order to regulate gene transcription and gene expression in a plants, in particular Eucalyptus grandis and Pinus radiata. The press invention describes DNA constructs containing DNA encoding a transcription factor that regulates the promoter, which is operably
                                                                                                                                                                                                                This invention relates to novel isolated plant nucleic acid molecules, variants thereof, that encode transcription factors. Specifically, it refers to transcription factor proteins that are capable of binding to
                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               polynucleotides isolated from plants encoding polypeptides encoded by such polynucleotides,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transcription and gene expression.
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Veerakone S,
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Lasham A, Lund
Westwood C,
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e K, Wood
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                                       Query Match
                                                                                                                 transgenic plants expressing a transcription factor that confers a trait to the plant such as increased drought, salt or disease tolerance, height change, enhanced cold/ frost tolerance, enhanced color, health and nutritional characteristics, as well as improved taste, starch composition, flower longevity and germination, amongst others. Accordingly, such plants that are successfully transfected with a DNA construct can be characterized by a difference in flower color, petal or leaf shape and size, aroma or plant height. This polypeptide is a plant transcription factor protein sequence of the invention.
                     Local
                                                                                662
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               33.9%;
                   Score 56;
Pred. No.
                     2.2e+02
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                                       Length 662;
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Best Loc
Matches
18
                    3 GNLGNNVNGNHLIPPAPPLPSQTDGA 28
                                       l Similarity
 GGVGDNNNGGYLHSPLSVMPLKSDGS 106
                                        Conservative
                                        Mismatches
                                          9
                                          Indels
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RESULT 28
ADT58973
ID ADT58
                                                                                                                     disease resistance; galactomannan production; plant growth heat tolerance; herbicide tolerance; lignin production; extreme osmotic condition tolerance; pathogens resistance; pest resistance; yield improvement; seed oil yield; seed p
                                                                              Viridiplantae.
                                                                                                                                                                                                 Plant; transgenic; cold tolerance;
                                                                                                                                                                                                                                            Plant polypeptide,
                                                                                                                                                                                                                                                                                                                                                                   ADT58973 standard; protein;
28-OCT-2004
                                      US2004216190-A1
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                                                                                                                                                                                                     growth rate;
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                                                                                                                     protein yield.
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genetics, and in particular biological characteristics. New recombinant DNA constructs useful in the field of biochemistry and for producing transgenic plants improved

WPI; 2004-757369/74.

28-APR-2003; 28-APR-2003;

2003US-00424599. 2003US-00425115.

(KOVA/) KOVALIC D

18-DEC-2003; 2003US-00739930

2; SEQ ID NO 9050; 14pp; English

polynucleotide having any of 5544 nucleotide sequences (CDNAs SEQ ID NO: 1-5544) and encoding a polypeptide with any of 5544 amino acid sequences (SEQ ID NO: 5545-11088). The cDNAs and proteins are from corn, soybean, Arabidopsis, wheat and rape but the specification does not indicate which sequences is derived from which organism. Also included is a method of producing a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising a promoter region functional in a plant cell operably joined to a polynucleotide encoding a polypeptide associated with the property, and growing the transformed plant. The property is selected from improving plant cold tolerance, for manipulating growth rate in plant cells by modification of the cell cycle pathway for improving plant cold received and polypeptide associated with the property. The invention relates a recombinant DNA construct comprising improving plant drought tolerance, for providing D increased

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RESULT 29
AEF21139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC resistance to plant disease, for galactomannan production, for production CC improving plant regulators, for improving plant tolerance, for improving plant tolerance, for comproving plant tolerance, for comproving plant tolerance, for improving the rate of the complex plant tolerance to extreme osmotic conditions, for improving the rate of complex plant tolerance to pathogens or pests, for yield improvement by modification of conditions, for improving plant compositions of pests, for modification of carbohydrate, nitrogen or phosphorus use and/or content, for modification of carbohydrate, nitrogen or phosphorus use and/or uptake and for yield improvement by providing improved plant growth and compositions of coverance to plant transcription factor. The methods and compositions of the present invention are useful in the field of biochemistry and composition are useful in the field of biochemistry and composition are useful in the field of biochemistry and composition are useful in the field of biochemistry and composition are useful in the field of biochemistry and composition are useful in the field of biochemistry and composition are useful in the field of biochemistry and composition of a plant tolerance to cold or heat, improved plant tolerance to plant pasts or pathogens. They can also be used in physical conterance to plant pasts or pathogens. They can also be used in physical arrays of molecules, plant breeding markers, computer-based storage and composition of pathogens. The present sequence is one of the 5544 plant protein sequences of the invention. Note: The sequence data for this patent did composition format directly from USPTO at sequence format directly from USPTO at sequence of the invention.
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Best Local Similarity
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Screening a modulator of a component involved in actin polymerization, comprises using pyrene- or acrylodan-globular actin, Arp2/3 complex, nucleation promoting factor, and an upstream regulator.
                                                                                                         WPI; 2006-077959/08.
                                                                                                                                                       Tomasevic N,
                                                                                                                                                                                                                                                         10-JUN-2004; 2004US-0578949P.
20-APR-2005; 2005US-0673444P.
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                                                                                                                                                                                                         (CYTO-) CYTOKINETICS INC.
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                                                                                                                                                       Sakowicz
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PRINTER TO THE PRINTE

Example 11; SEQ ID NO

47; 106pp; English

Claim 2; SEQ ID NO 10284; 14pp; English

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                                                               New recombinant DNA constructs useful in the field of biochemistry and genetics, and in particular for producing transgenic plants with improviological characteristics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disease resistance; galactomannan production; plant growth heat tolerance; herbicide tolerance; lignin production; extreme osmotic condition tolerance; pathogens resistance; pest resistance; yield improvement; seed oil yield; seed pr
                                                                                                                                                                                                                                     WPI; 2004-757369/74
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28-APR-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plant polypeptide, SEQ ID 10284.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADT60207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; protein; 319 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2003US-00424599.
2003US-00425115.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            $
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 55.5;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .4e+02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1:
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RESULT 31
ABU37030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
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21-MAR-2001;
06-SEP-2001;
25-OCT-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          producing a plant having an improved property, comprising transforming a plant with a recombinant DNA construct comprising a promoter region functional in a plant cell operably joined to a polynucleotide encoding a polypeptide associated with the property, and growing the transformed plant. The property is selected from improving plant cold tolerance, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for improving plant drought tolerance, for providing increased resistance to plant disease, for galactomannan production, for production of plant growth regulators, for improving plant tolerance, for improving plant tolerance to herbicides, for increasing the rate of homologous recombination in plants, for lignin production, for improving plant tolerance to extreme osmotic conditions, for improving plant
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                                                                                                                                                   21-MAR-2002; 2002WO-US009107.
                                                                                                                                                                                                                                                                                                          WO200277183-A2
                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense; prokaryotic essential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein encoded by Prokaryotic essential gene #22557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABU37030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABU37030 standard; protein; 598 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VPPPPPVPGAPDAAAR 40
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2001US-00815242
2001US-00948993
2001US-0342923P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene; cell proliferation; drug design
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29-JUL-2004 AB077698;

(first entry

Pseudomonas aeruginosa polypeptide #9873.

Bacterial infection; Pseudomonas aeruginosa infection; antibacterial

Pseudomonas aeruginosa

RESULT 32

ABO77698 standard; protein; 631 AA

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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

((1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense concleic acid; (4) a host cell containing the vector; (3) an isolated containing the vector; (3) an isolated containing the polypeptide by the inding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway crequired for proliferation, or that inhibits cellular proliferation or the biological pathway in which a proliferation, or that inhibits cellular proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent constitute activity activity of a culture of activity of a culture or collucation of an organism; or (13) identifying the target of a compound that inhibits the collular proliferation of an organism; or (13) identifying the target of a compound that inhibits the collular proliferation of an organism. The antisense nucleic acids are useful for identifying proliferation to isolate candidate molecules for rational confidence of the strains or screening for homologous nucleic acids required for cellular proliferation for arrange or for arrange and antisense nucleic acids are sectored to incompound that inhibits the confidence and inference or for arrange and antisense nucleic acids are useful for collular proliferation to isolate candidate molecules for rational confidence and incompound that inhibits and antisense nucleic acids are confidented.
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Matches
                                                                                                                                    Query Match
                                                                                                                                                                                                                                                       drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-FEB-2002; 2002US-00072851
06-MAR-2002; 2002US-0362699P
                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 25; SEQ ID NO 64954; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to
                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isolate candidate molecules for rational drug discovery programs
                                                                                                                госат
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to an isolated nucleic acid comprising 6213 antisense sequences given in the specification where
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343
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Trawick JD,
NNVPPSPPIPPAPPPSGLD
                                            NNVNGNHLIPPAPPLPSQTD
                                                                                             Conservative
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Carr GJ,
                                                                                                              33.3%;
                                                                                        Score 55; DB 6; Le
Pred. No. 2.7e+02;
1; Mismatches 7;
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Forsyth
                                                                                                                                         Length 598;
                                                                                             Indels
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Xu HH;
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                                                                                                                                                                                                                                                                                                                            typhimurium,
                                                                                             Gaps
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ABM86049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to Pseudomonas aeruginosa polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and the therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of concluding anti-P. aeruginosa drugs, as targets for antibacterial drugs, concluding anti-P. aeruginosa drugs, as templates for recombinant conduction of P. aeruginosa drugs, as templates for recombinant conduction of P. aeruginosa drugs, as templates or polypeptides, as target components for diagnosis and/or treatment of P. aeruginosa-caused components for diagnosis and/or treatment of P. aeruginosa-caused components for diagnosis and/or treatment of P. aeruginosa-caused confection, and in detection of P. aeruginosa sequences or other sequences of Pseudomonas species using biochip technology. Sequences ABO67826-CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 10
22-JUN-2001; 2001US-0300112P
24-AUG-2001; 2001US-0314662P
                                                                                                                                        Oryza sativa
                                                                                                                                                                     abiotic stress
                                                                                                                                                                                                   Rice abiotic stress responsive polypeptide SEQ ID NO:4295
                                                                                                                                                                                                                                     02-JUN-2005
                                                                                                                                                                                                                                                                                               ABM86049 standard; protein; 899
                                            21-JUN-2002; 2002WO-US019668
                                                                                                          WO2003008540-A2
                                                                                                                                                                                                                                                                      ABM86049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 631 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seqdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 26444; 455pp; English
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27-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                 397
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                                                                                                                                                                                                                                                                                                                                                                              NSLPGNPSTPPTPPLPVQ
                                                                                                                                                                                                                                                                                                                                                                                                          NNVNGNHLIPPAPPLPSQ 24
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                    (first
                                                                                                                                                                  tolerance; transgenic plant; plant; cereal; agriculture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nolling J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        THERAPEUTICS
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98US-0094190P
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                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 55; DB Pred. No. 2.8e 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ب</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                    2.8e+02;
6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 631
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Best Local
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          WPI; 2001-656860/75
N-PSDB; ABL12354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to novel abiotic stress responsive polynucleotides and polypeptides. Also disclosed are vectors, expression cassettes, host cells, and plants containing such polynucleotides. Also disclosed are methods for using the polynucleotides and polypeptides to alter the responsiveness of a plant to abiotic stress. The invention is useful in agriculture. The nucleic acid is useful for determining whether a test plant has been exposed to an abiotic stress condition. It is also useful for selecting an agent that alters abiotic stress regulated polynucleotide expression in a plant cell, and to identify a homolog or ortholog to an abiotic stress responsive polynucleotide. The nucleic acid molecule and the polypeptide encoded by it are useful in altering the responsiveness of a plant to an abiotic stress, such as cold stress, salt stress, canting the stress, canting the stress are combinations. The present sequence is used in the exemplification of their combinations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New stress-responsive nucleic acid, useful responsiveness of a plant, e.g. cereal, to stress, salt stress or osmotic stress.
                                                                                                             23-MAR-2000; 2000US-0191637P.
11-JUL-2000; 2000US-00614150.
                                                                                                                                                                                                                                            Drosophila melanogaster
                                                                                                                                                                                                                                                                          pharmaceutical.
                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster polypeptide SEQ ID NO 31545
                                                                                                                                                                                                                                                                                                                                                  26-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 899 AA;
                                                     Venter JC,
                                                                                                                                                       23-MAR-2001; 2001WO-US009231.
                                                                                                                                                                                     27-SEP-2001.
                                                                                                                                                                                                                  WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                                               ABB68251;
                                                                                                                                                                                                                                                                                                                                                                                                        ABB68251 standard; protein; 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 4295; 89pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kreps J, Briggs SP, Cooper B,
Moughamer T, Provart N, Ricke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-SEP-2001; 2001US-0325277P.
21-NOV-2001; 2001US-0332132P.
                                                                                  (PEKE ) PE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
7; Conserv
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                                                                                  CORP NY
                                                     Adams M,
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                                                     PWD,
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Pred. No.
                                                     Myers EW
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D, Zhu T;
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ABO74627
ID ABO74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                            The invention relates to Pseudomonas aeruginosa polypeptides and the polynuclectides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection, for evaluating a compound, such as a polypeptide, for the ability to bind a P. aeruginosa nucleic acid, as components of
                                                                                                                                                                                                       Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
              effective antibacterial targets, as targets for antibacterial drugs, including anti-P. aeruginosa drugs, as templates for recombinant
                                                                                                                                                                       Disclosure; SEQ ID NO
                                                                                                                                                                                                     pathological
                                                                                                                                                                                                                                                                                                                            Rubenfield
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27-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacterial infection; Pseudomonas aeruginosa infection; antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas aeruginosa polypeptide #6802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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                                                                                                                                                                                                                                                                                                                                                                GENOME
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98US-0094190P.
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aeruginosa-derived
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Pred. No. 1.4e
3; Mismatches
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peptides
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es 3;
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polypeptides,
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target
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             biodiversity assessment; Parkinson's disease; Ālzheimēr's disease; neurodegenerative diseases; anaemia; platelet disorder; wound; burns; ulcers; osteoporosis; autoimmune disease; cancer; molecular weight marker; food supplement; antiparkinsonian; nootropic; neuroprotective; antinaemic; anticoagulant; thrombolytic; vulnerary; neuroprotective; antinaemic; anticoagulant; thrombolytic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection, and in detection of P. aeruginosa sequences or other sequences of Beeudomonas species using biochip technology. Sequences ABO67826-ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPTO at
                                                                                                                                                               New polynucleotide and polypeptide useful for diagnosing, preventing or treating conditions such as neurodegenerative diseases, anemias, platelet disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                              WPI; 2003-371981/35.
                                                                                                                                                                                                                                                                Tang TY, Zhang J,
Zhou P, Ghosh M,
                                                                                                                                                                                                                                                                                                                               24-SEP-2001; 2001US-0324631P
                                                                                                                                                                                                                                                                                                                                                       24-SEP-2002; 2002WO-US030474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human novel polypeptide sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADC30973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     segdata.uspto.gov/sequence.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                components for diagnosis and/or treatment of P. aeruginosa-caused
                                                                                                                                                                                                                 N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                 10-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiulcer; osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; diagnostic; drug screening; forensics;
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                                                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                        therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome
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Wang D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunosuppressive; antiinflammatory; cytostatic;
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                                                                                                                                                                                                                                                                  Xue AJ, Zhao
Ma Y, Asundi
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Pred.
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The invention relates to 971 novel human cDNA sequences (ADC29919-ADC30889) and the polypeptides they encode (ADC30890-ADC31860). The invention also relates to nucleic acid sequences over 99% identical with the novel human cDNAs. The invention additionally encompasses expression vectors and host cells comprising a nucleic acid of the invention; the recombinant production of a polypeptide of the invention; an antibody against a polypeptide of the invention, a method of detecting polynucleotides or polypeptides of the invention; and methods of identifying a compound which binds to a polypeptide of the invention. The

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disorders, wounds, burns, ulcers, osteoporosis, autoimmune

Claim

20; SEQ ID NO 1055; 1185pp; English

The section of

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CC invention further discloses methods of peventing, treating or CC ameliorating a medical condition; kits comprising polynucleotide probes CC and/or monoclonal antibodies for carrying out the methods of the CC invention; methods for the identification of compounds that modulate the CC invention; methods for the identification of compounds that modulate the CC contig sequences corresponding to the CDNA sequences of the invention CC (ADC31861-ADC32827) and the polypeptides encoded by the contigs (ADC32628 and EDC3394). The nucleic acids and polypeptides of the invention are CC useful in diagnostics, drug screening, forensics, gene mapping, in the CC identification of mutations responsible for genetic disorders or other traits, for assessing biodiversity, and in producing many other types of CC data and products dependent on DNA and amino acid sequences. They are CC also used for treating diseases such as Parkinson's disease, Alzheimer's CC disease and other neurodegenerative diseases, anaemia, platelet CC disorders, wounds, burns, ulcers, osteoporosis, autoimmune diseases or CC primers, and in the recombinant production of a protein. The polypeptides are also useful in generating antibodies, as molecular weight markers, CC and as food supplements. The present sequence represents a specifically CC claimed human polypeptide sequence of the invention. Note: The sequence CC was obtained in electronic format directly from WIPO at CC tro, wibo. int/oub/published not sequences.
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Best Local
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(GIET/)
(CHIN/)
(DUFO/)
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17-JAN-2002; 2002US-0349946P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Antiarteriosclerotic; antipsoriatic; cytostatic; secretory molecule; agonist; antagonist; gene therapy; antisense; human; secretory; purified secretory polynucleotide; sptm; toxicity; arteriosclerosis; psoriasis; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human purified secretory polypeptide (SPTM), seq
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                                                                                                                                                                                                                                                                                                                                                             (INCY-)
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                                                                                       GIETZEN D.
CHINN J.
DUFOUR G E.
JACKSON J L.
YU J Y.
TURSON O.
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AMSHEY S R.
DAM T C.
                                                                                                                                                                                                                                                                                          JONES A L.
DAHL C R.
                                                                                                                                                                                                                                                                                                                                                          INCYTE GENOMICS INC
                                                            YAP PE.
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Pred. No. 1.2e+02;
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RESULT 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to isolated purified secreted polynucleotides (SpTM) (1), and the polypeptides (SpTM) encoded by sptm. A polypeptide encoded by (I) is used to identify a compound which binds to it. A microarray comprising (I) is used to generate a transcript. (I) is used to screen a compound for effectiveness in altering expression of (I). (I is used to assess toxicity of a test compound. An agonist or antagonist identified by a new method is used in a pharmaceutical composition. The secretory molecules are used to diagnose or treat conditions, diseases o disorders associated with cell signaling e.g. arteriosclerosis, psoriasis, and cancer. Sequences given in ADI40308-ADI40468 represent human purified secretory polynucleotides of the invention, and those given in ADI40469-ADI40461 represent the polypeptides they encode.
                                                                                                      12-APR-2002; 2002EP-00008400
                                                                                                                                                                                                               EP1347046-A1
                                                                                                                                                                                                                                                                                                                        human; gene therapy; diagnostic marker; pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                           Human protein of the invention SEQ ID NO:4737.
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                                                22-MAR-2002; 2002JP-00137785.
                                                                                                                                                            24-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADM06052 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 27a; SEQ ID NO 219; 486pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated secreted polynucleotide for diagnosing or treating conditions, diseases or disorders associated with cell signaling e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-853444/79.
N-PSDB; ADI40363.
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(GERS/)
(PERA/)
(REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arteriosclerosis, psoriasis, and cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kristnam SR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Match 32.7%;
Local Similarity 47.6%;
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JY, Tuason O, Yap ...
calta CH, Lewis SA, Che
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10;
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GERSTINEH.
PERALTACH.
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ason O, Yap PE, Amshey SR, Dam TC, Liu TF, Gerstin
, Lewis SA, Chen AJ, Marwaha R, Lan RY, Urashka ME;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
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Pred. No.
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RESULT 39
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                          Homo
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Yamamoto J, Isono Y,
Seki N, Yoshikawa T,
   osteoporosis,
                         New
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12-APR-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                stomach ulcer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Osteopathic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cDNA clone protein TKIDN20005210,
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                                                                                                                                                         Isogai T,
                                                                                                                                                                                               (REAS-)
full-length cDNA sequences, useful for treating diseases, e. soporosis, cancer, inflammation, gastritis, or gastroduodenal
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                                                                             2005-667421/69
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                                                             AEC86539.
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                                                                                                                 Yoshikawa
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                                                                                                                                     Sugiyama T,
, Isono Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene
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                                                                                                                                                                                             ASSOC BIOTECHNOLOGY.
                                                                                                                                                                                                                                 2002JP-00137785.
2002EP-00008400.
                                                                                                                                                                                                                                                                                          2004EP-00027348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cytostatic; Antiinflammatory; ene Therapy; Osteoporosis; cand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                              gastrointestinal ulcer.
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Hio Y, Otsuka K, Nagai K, Irie
Otsuka M, Nagahari K, Masuho Y;
                                                                                                               Otsuki T, Wakamatsu A,
Hio Y, Otsuka K, Nagai
Otsuka M, Nagahari K, N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer; inflammation; gastritis;
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                                                                                                                   Masuho
                                                                                                                                 Sato H, Is
K, Irie R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                     Tamechika
                 e.g.
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   ulcer
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The invention describes a recombinant DNA construct comprising polynucleotide consisting of a sequence encoding an amino acid available in electronic form from the US patent office at ftp.seqdata.uspto.gov/sequence.html?DocID:2004034888. The polyn

polynucleotide

sequence

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RESULT 40
AD724521
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                                                                                                                                                                                                                                                                                      New recombinant DNA construct, useful for improving plant tolerance cold, heat, drought, herbicides, extreme osmotic conditions, pathoge pests, for conferring increased resistance to plant disease, or for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ZHOU/)
(KOVA/)
(SCRE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              plant protectant; plant growth regulant; gene therapy; plant;
recombinant DNA construct; physical array; plant breeding marker;
cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-MAY-1999;
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yield; plant growth; plant development; seed oil; protein yield;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TABA/)
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Query Match 32.7%; Score 54; DB 8; Length 319
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Matches 10; Conservative 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                        of the invention are also useful in physical arrays of molecules and as plant breeding markers. The recombinant DNA construct is useful for improving plant tolerance to cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or pests, for manipulating growth rate in plant cells by modification of the cell cycle pathway, for conferring increased resistance to plant disease, for producing galactomannan, lignin or plant growth regulators, for increasing the rate of homologous recombination in plants, for improving yield by modification of photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake or by providing improved plant growth and development under at least one stress condition or for modifying seed oil or protein yield and/or content. This is the amino acid sequence of a plant full length insert polypeptide that can be used in the recombinant DNA construct of the
                                                                                                                                                                                                                        Sequence 319 AA;
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Q2W1P9_MAGSA
Q2QW44_ORYSA
Q4DJY5_TRYCR
Q4DJY5_TRYCR
Q4DJY5_TRYCR
Q4DJY5_TRYCR
Q2S32B_95EHI
Q6FUB5_HUMAN
Q4DJY5_TRYCR
Q2S32B_95EHI
Q6FUB5_HUMAN
Q5FLJ8_CANBL
Q5FLJ8_CANBL
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Q5FUB5_MOUSE
Q5FUB5_CABEL
Q5FUB7_CABEL
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MEDLINE=98254123; PubMed=9593291;
Elliott S.J., Wainwright L.A., Mc
Lai L.C., McNamara B.P., Donnenbe
                                                                                                                   Bacteria; Proteobacteria;
Enterobacteriaceae; Eschei
                                                                                                                                                    Escherichia
                                                                                                                                                                                                      07-FEB-2006,
                                                                                                                                                                                                                  01-JUN-1998,
01-JUN-1998,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF013122; AAB88410.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stein M.S., Kenny B., Finlay B.B.; Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=E2348/69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        adherence into mammalian cells."; Cell 91:511-520(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=E2348/69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Escherichia.
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07-FEB-2006,
                                                     STRAIN=E2348/69;
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                                                                   NUCLEOTIDE SEQUENCE.
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CO:0007155; P:cell adhesion; IEA.
InterPro; IPR003536; Tir rcpt.
Eam; PF07489; Tir receptor C; 1.
Eam; PF03549; Tir receptor M; 1.
Eam; PF07490; Tir receptor N; 1.
RINTS; PR01370; TRNSINTIMINR.
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L.A., McDaniel T.K.,
Donnenberg M.S., Kap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MW.
                                                                                                                                 Gammaproteobacteria;
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Pred. No. 5.3e-12;
; Mismatches 0;
                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; DOI=10.1016/S0092-8674(00)80437-7; Reinscheid D.J., Frey E.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IEA.
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   .K., Jarvis K.G.,
Kaper J.B.;
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RESULT 3
OSWMC9 ECOLI
ID QSWMC9 ECOLI
ID QSWMC9,
AC QSWMC9,
DT 23-NOV-2
DT 23-NOV-2
DT 23-NOV-2
DT 23-NOV-2
DT 33-NOV-2
DT 33-NOV-2
DT 33-NOV-2
DT 13-NOV-2
DT 13-ING
RE NUCLEOTI
RC STRAIN-C
RX PUBMEd-I
RA Gartner
RT "Compara
RT Islands
RI Gartner
RT "Compara
RA Gartner
RT "Etablic
RT molekulk
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Q5WMC9;
23-NOV-2004,
23-NOV-2004,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003536; Tir_rcpt.
Pfam; PF07489; Tir_receptor_G;
Pfam; PF03549; Tir_receptor_N;
Pfam; PF07490; Tir_receptor_N;
PRINTS; PR01370; TRNSINTIMINR.
                                                                                                                                                                                                                                                                                                                                                                                                                      "Etablierung eines Zellkulturmodells fuer M-Zellen und vergleichende
molekulare Analyse der LEE-Pathogenitaetsinsel atypischer
enteropathogener Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=15501811; DOI=10.1128/IAI.72.11.6722-6728.2004; Gartner J.F., Schmidt M.A.; "Comparative Analysis of Locus of Enterocyte Effacement Pathogenicity Islands of Atypical Enteropathogenic Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/termsDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The complete sequence of the locus of enterocyte effacement from enteropathogenic Escherichia coli E2348/69."; Mol. Microbiol. 28:1-4(1998).
                                                                            Pfam; PF07489; Tir_receptor_C;
Pfam; PF03549; Tir_receptor_N;
Pfam; PF07490; Tir_receptor_N;
                                                                                                                                            GO; GO:0004872; F:receptor activity; GO; GO:0007155; P:cell adhesion; IEA InterPro; IPR003536; Tir rcpt.
                                                                                                                                                                                                                            EMBL; AJ633129; CAG17536.1; -; Genomic_DNA.
SMR; Q5WMC9; 272-336.
                                                                                                                                                                                                                                                                                                                                                                        Thesis (2002), Department of Biological Sciences, University Muenster, Muenster, Germany.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaertner J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=0181-6/86;
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                                                     PRINTS; PR01370; TRNSINTIMINR
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Pred. No. 5.3
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          126029D6C070E9BB CRC64;
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Attribution-NoDerivs License
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RESULT 4
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Best Local Similarity
Matches 30; Conser
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GO; GO:0004872; F:receptor activity; IE
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR003536; Tir_ropt
Pfam; PF07489; Tir_receptor_C; 1.
Pfam; PF07490; Tir_receptor_M; 1.
Pfam; PF07490; Tir_receptor_N; 1.
PRINTS; PR01370; TRNSINTININR.
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01-AUG-1998,
01-AUG-1998,
                             (1)
NUCLEOTIDE SEQUENCE.
NEDLINE=98187918; PubMed=9529069;
MEDLINE=98187918; PubMed=9529069;
Voss E., Paton A.W., Manning P.A., Paton J.C.;
Voss E., Paton A.W., Manning P.A., Paton J.C.;
"Molecular analysis of Shiga toxigenic Escherichia
syndrome.
.Infect. I
[2]
                                                                                                                                                                                                                                                                                                01-AUG-1998, sequence version 07-FEB-2006, entry version 19. Translocated intimin receptor.
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                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammar
Enterobacteriaceae; Escherichia
                                                                                                                                                                                                                                                                               Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB036053; BAA96815.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
                                                                                                                                                                                                           NCBI_TaxID=562;
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                        66:1467-1472(1998)
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No. 5.3e-12;
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                                                                      hemolytic-uremic
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Q4ZIMO_ECOLI
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Best Local S
Matches 27
               EMBL; DQ007024; AAY25395.1; -; Genc EMBL; DQ007022; AAY25393.1; -; Genc SMR; Q4ZIM0; 272-336.

GO; GO:00004872; F:receptor activity GO; GO:0007155; P:cell adhesion; II InterPro; IPR003536; Tir_rcpt.
Pfam; PF07489; Tir_receptor_C; 1.
Pfam; PF07490; Tir_receptor_N; 1.
PRINTS; PR01370; TRNSINTIMINR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-2005,
07-JUN-2005,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
STRAIN=CPG124 WC416, and CPG123-G58;
PubMed=16272509; DOI=10.1128/JCM.43.11.5715-5720.2005;
Garmendia J., Ren Z., Tennant S., Midolli Viera M.A., (
Whale A., Azzopardi K., Dahan S., Sircili M.P., Franzol
Trabulei L.R., Phillips A., Gomes T.A., Xu J., Robins-
                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/teDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                J. Clin.
                                                                                                                                                                                                                                                                                                                                                                                       Enteropathogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Name=tir;
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Q4ZIMO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterobacteriaceae;
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Infect. Immun. 66:5580-5586(1998).
                                                                                                                                                                                                                                                                                                                                                                            "Distribution of tccP in Clinical Enterohemorrhagic Enteropathogenic Escherichia coli Isolates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                       Frankel G.;
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Escherichia.
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Genomic_DNA.
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Franzolin
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RESULT 8
Q7BHL5 9ENTR
ID Q7BHL5 9
AC Q7BHL5 - 2
DT 05-JUL-2
DT 05-JUL-2
DT 07-FEB-2
DT Transloc
OS Citrobac
OC Enterobac
OC Enterobac
OC MCGI_Tax
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Q4ZIM1;
07-JUN-2005,
07-JUN-2005,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Receptor.
SEQUENCE
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                          NCBI_TaxID=67825;
                                                        Enterobacteriaceae;
                                                                                Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                              Citrobacter rodentium.
                                                                                                                                      05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 8.
Translocated intimin receptor Tir.
                                                                                                                                                                          05-JUL-2004, integrated into UniProtKB/TrEMBL 05-JUL-2004, sequence version 1. 07-FEB-2006, entry version 8.
                                                                                                                                                                                                                                                           Q7BHL5_9ENTR
Q7BHL5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam, PF07489; Tir_receptor_G; 1.
Pfam; PF03549; Tir_receptor_M; 1.
Pfam; PF07490; Tir_receptor_N; 1.
PRINTS; PR01370; TRNSINTIMINR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; DQ007023; AAY25394.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Distribution of tccP in Clinical Enterohemorrhagic Enteropathogenic Escherichia coli Isolates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Frankel G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=16272509; DOI=10.1128/JCM.43.11.5715-5720.2005; Garmendia J., Ren Z., Tennant S., Midolli Viera M.A., Chor Whale A., Azzopardi K., Dahan S., Sircili M.P., Franzolin Trabili L.R., Phillips A., Gomes T.A., Xu J., Robins-Brow
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 149; DB 2; Pred. No. 5.3e-10; Mismatches 1;
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Pred. No. 5.3e-10;
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                                                                                      Enterobacteriales;
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SEQUENCE
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RESULT 9

QPETI1 9ENTR

ID QPETI1;

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DT 01-MAR-2001, i

DT 01-MAR-2001, i
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HSSP; Q9KWH9; 1F02.
SNR; Q9E7I1; 270-334.
SNR; Q9E7I1; 270-334.
GO; GO:0004872; F:receptor activity; IEP
R GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPRO03536; Tir rept.
R Pfam; PF07489; Tir receptor C; 1.
Pfam; PF03549; Tir receptor M; 1.
Pfam; PF03549; Tir receptor N; 1.
Pfam; PF03549; Tir receptor N; 1.
OR Pfam; PF03549; Tir receptor N; 1.
OR Pfam; PF03549; Tir receptor N; 1.
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Pfam; PF03549; Tir_receptor_M;
Pfam; PF07499; Tir_receptor_N;
PRINTS; PR01370; TRNSINTIMINR.
                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=CDC 1843-73T, and DBS100;
MEDLINE=20553330; PubMed=11101562;
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DOI=-10.1128/IAI.69.10.6323-6335.2001;
Deng W., Li Y., Vallance B.A., Finlay B.B.;
"Locus of enterocyte effacement from Citrobacter rodentium; sequence
                                                                                                                                                                                                             EMBL; AF301618; AAG40758.1; -; Genomic_DNA.
EMBL; AF301617; AAG25642.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                              colonic hyperplasia, exhibits clonality: synonymy
mouse-pathogenic Escherichia coli.";
J. Clin. Microbiol. 38:4343-4350(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE.
STRAIN=CDC 1843-73T,
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GO; GO:0007155; P:cell adhesio
InterPro; IPR003536; Tir_rcpt.
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Pred. No. 7.1e-08;
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CB8318B301049C37 CRC64;
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RESULT : Q9WXX1 | Q9W
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Best Local S
Matches 25
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SMR; Q9WXK1; 270-334.

GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR003536; Tir_rcpt.
Pfam; PF07489; Tir_receptor_C; 1.
Pfam; PF03549; Tir_receptor_N; 1.
Pfam; PF07490; Tir_receptor_N; 1.
PRINTS; PR01370; TRNSINTIMINR.
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085506_ECOLI
085506
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SEQUENCE
MEDLINE-99003184; PubMed-9784578;
Paton A.W., Manning P.A., Woodrow M.C., Paton J.C.;
"Translocated intimin receptors (Tir) of Shiga-toxigenic
                                                                                                                                                                                                                                                                     01-NOV-1998, integrated into UniProtKB/TrEMBL.
01-NOV-1998, sequence version 1.
07-FEB-2006, entry version 18.
Translocated intimin receptor Tir.
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01-NOV-1999, integrated into U
01-NOV-1999, sequence version
07-FEB-2006, entry version 16.
Translocated intimin receptor.
                                                                                                                                                                                                                        Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Okutani A., Itoh K., Sasakawa C.; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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                                                                                                                                               NCBI_TaxID=562;
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25; Conserv
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Pred. No. 7.1e-08;
1; Mismatches 4
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Pred. No. 7.1e-08;
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RESULT 12
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ID Q4ZIM4_E
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Best Local &
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EMBL; DQ007019; AAY25390.1; -; Genomic_DNA.
SMR; Q4ZIM4; 271-335.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:000155; P:cell adhesion; IEA.
InterPro; IPR003536; Tir_rcpt.
Pfam; PF07489; Tir_receptor_C; 1.
Pfam; PF07549; Tir_receptor_M; 1.
Pfam; PF07490; Tir_receptor_N; 1.
PRINTS; PR01370; TRNSINTIMINR.
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GO; GO:0007155; P:cell adhesion;
InterPro; IPR003536; Tir rcpt.
Pfam; PF07489; Tir receptor C; 1.
Pfam; PF07549; Tir receptor M; 1.
Pfam; PF07490; Tir receptor N; 1.
PRINTS; PR01370; TRNSINTIMINR.
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Q4ZIM4;
07-JUN-2005,
07-JUN-2005,
07-FEB-2006,
                                                                                                Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CPG122-G57, and CPG6;
PubMed=16272509; DOI=10.1128/JCM.43.11.5715-5720.2005;
PubMed=16272509; DOI=10.1128/JCM.43.11.5715-5720.2005;
Garmendia J., Ren Z., Tennant S., Midolli Viera M.A., Chong Whale A., Azzopardi K., Dahan S., Sircili M.P., Franzolin M. Whale A., Azzopardi K., Dahan S., Sircili M.P., Robins-Browne Craphilsi L.R., Phillips A., Gomes T.A., Xu J., Robins-Browne
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Distribution of tccP in Clinical Enter
Enteropathogenic Escherichia coli Isola
J. Clin. Microbiol. 43:5715-5720(2005).
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Escherichia coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Frankel G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Translocated
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Best Local Similarity
                                                                                                           GO; GO:0004872; F:receptor activity; II
GO; GO:0004872; F:receptor activity; II
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR003536; Tir receptor C; 1.
Pfam; PF07489; Tir receptor M; 1.
Pfam; PF07490; Tir receptor N; 1.
PRINTS; PR01370; TRNSINTIMINR.
                                                                                                                                                                                                                                                                                                            PIR; A98199; A98199.
PIR; E86045; E86045.
HSSP; Q9KWH9; 1F02.
SMR; Q9R396; 269-333.
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01-MAY-2000,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
STRAIN-ATCC43895, and EDL933;
MEDLINE-98339885; pubMed=9673266;
Perna N.T., Mayhew G.F., Posfai G., Elliott S.,
Kaper J.B., Blattner F.R.;
"Molecular evolution of a pathogenicity island
Escherichia coli O157:H7.";
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                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Distribution of tccP in Clinical Enterohemorrhagic Enteropathogenic Escherichia coli Isolates.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Frankel G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=16272509; DOI=10.1128/JCM.43.11.5715-5720.2005; Garmendia J., Ren Z., Tennant S., Midolli Viera M.A., Chor Whale A., Azzopardi K., Dahan S., Sircili M.P., Franzolin Trabulsi L.R., Phillips A., Gomes T.A., Xu J., Robins-Brow
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE
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GO; GO:0004875; P:receptor activity; I)
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR003536; Tir receptor
Pfam; PF07489; Tir receptor M; 1.
Pfam; PF07490; Tir receptor N; 1.
PRINTS; PR01370; TRNSINTIMINR.
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Q7DB77; Q7A901;
05-JUL-2004, integrated
05-JUL-2004, sequence v
07-FEB-2006, entry vers
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STRAIN=0157:H7 / EDL933 / ATCC 700927 / EBEZ;
MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7."
Nature 409:529-533(2001).
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STRAIN=0157:H7 / Sakai / RIMD 0509952 / EHEC;
MEDLINE=21156231; PubMed=11258796; DOI=10.1093/dnares/8.1.11;
MEDLINE=21156231; PubMed=11258796; DOI=10.1093/dnares/8.1.11;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama
Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; Gammaproteobacteria;
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                                                            MEDIINE=99003184; PubMed=9784578; Paton J.C.; Paton A.W., Manning P.A., Woodrow M.C., Paton J.C.; "Translocated intimin receptors (Tir) of Shiga-toxigenic Escherichia coli isolates belonging to serogroups O26, O111, and O157 react with sera from patients with hemolytic-uremic syndrome and exhibit marked sequence heterogeneity."; Infect. Immun. 66:5580-5586(1998).
                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
STRAIN=EPEC87A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1998, integrated into UniProtKB/TrEMBL
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Translocated intimin receptor.
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Hohn C., Karns J.S., Higgins J.A.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
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PubMed=15870341; DOI=10.1128/AEM.71.5.2511-2519.2005;
Higgins J.A., Belt K.T., Karns J.S., Russell-Anelli J.,
"tir- and stx-Positive Escherichia coli in Stream Water:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
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GO:0004872; F:receptor activity;
GO:0007155; P:cell adhesion; IEA
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Pred. No. 1e-06;
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)14_ECOLI
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Q47014;
01-NOV-1996,
Deibel C., Kraemer S., Chakraborty T., Ebel F.; "EspE, a novel secreted protein of attaching and effacing directly translocated into infected host cells where it ap tyrosine-phosphorylated 90 kDa protein."; Mol. Microbiol. 28:463-474(1998).
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SEQUENCE
                                                                                                                                                                                                                    DOI=10.1128/IAI.68.4.2171-2182.2000; Marches O., Nougayrede J.-P., Boullier S., Mainil J., Raymond I., Pohl P., Boury M., De Rycke J., Milon A., Raymond for and intimin in the virulence of rabbit en Escherichia coli serotype O103:H2."; Infect. Immun. 68:2171-2182(2000).
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Escherichia coli
                                                                                                                                                          STRAIN=413/89-1;
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07-FEB-2006,
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GO; GO:0004872; F:receptor
GO; GO:0007155; P:cell adhe
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HSSP; Q9KWH9; 11
                                                                                                                                                                                                                                                                                                                                                        WEDLINE=20187493; PubMed=10722617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE
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serogroups 026, 0111, and 0157 react with
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                             Elliott S.J., Wainwright L.A., McDaniel T.K., Jarvis Lai L.C., McNamara B.P., Donnenberg M.S., Kaper J.B.; "The complete sequence of the locus of enterocyte eff from enteropathogenic Escherichia coli E2348/69."; Mol. Microbiol. 28:1-4(1998).
                                                                                                                                                                                 STRAIN=RDEC-1;
MEDLINE=98254123;
                                                                                                                                                                                                                                                                                                                                                                             STRAIN=RDEC-1;
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Distributed under the Creative
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AP113597; AAF03080.1; -; Genomic_DNA.
AJ223063; CAA11065.1; -; Genomic_DNA.
AJ277443; CAC81869.1; -; Genomic_DNA.
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Pfam; PF07489; Tir_receptor_N;
Pfam; PF03549; Tir_receptor_N;
Pfam; PF07490; Tir_receptor_N;
PRINTS; PR01370; TRNSINTIMINR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SMR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21153569; PubMed=11254564;
DOI=10.1128/IAI.69.4.2107-2115.2001;
Zhu C., Agin T.S., Elliott S.J., Joh
 STRAIN=Gywnns Run Gwynnbrook stream; PubMed=15870341; DOI=10.1128/AEM.71.5.2511-2519.2005;
                                                                         Bacteria; Proteobacteria;
Enterobacteriaceae; Esche
                                                                                                     Escherichia coli
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EMBL; AF200363; AAK26722.1; -; Genomic_DNA.
EMBL; AF453441; AAL57549.1; -; Genomic_DNA.
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MEDLINE=97055784;
Agin T.S., Cantey
                              NUCLEOTIDE SEQUENCE.
                                                          NCBI_TaxID=183192;
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pubMed=15870341; DOI=10.1128/AEM.71.5.2511-2519.2005;
Higgins J.A., Belt K.T., Karns J.S., Russell-Anelli J.,
"tir- and stx-Positive Escherichia coli in Stream Water;
Metropolitan Area.";
Metropolitan Area.";
71.2611-2610/2005)
           GO; GO:0004872; F:receptor activity; GO; GO:0007185; P:cell adhesion; IEA. InterPro; IPG03536; Tir_rect. Pfam; PF07489; Tir_receptor_C; 1. Pfam; PF07490; Tir_receptor_N; 1. Pfam; PF07490; Tir_receptor_N; 1.
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Hohn C., Shelton D.R., Higgins J.A.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
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Metropolitan Area.";
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GO:0004872; F:receptor activity;
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erPro; IPR003536; Tir_rcpt.
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MEDLINE-21538660; PubMed=11682182;

JOTES J., Rumer L., Kiessling S., Kaper J.B., Wieler L.H.;

"Identification of a new pathogenicity island inserted in the pheV

"Identification of a new pathogenicity island inserted in RM1374

"ERNA gene of the bovine Shiga toxin-producing E. coli strain RW1374

"ERNA gene of the bovine a locus of enterocyte effacement that is flanked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q5K5P9_ECOLI
Q5K5P9;
15-FEB-2005,
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Q5K5P9_I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor.
SEQUENCE
                                                                 GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPo; IPR003536; Tir rept.
Pfam; PF07489; Tir receptor M; 1.
Pfam; PF07490; Tir receptor N; 1.
Pfam; PF07490; Tir receptor N; 1.
                                                                                                                                                                      SMR:
                                                                                                                                                                                                                                                                virulence features in the enterchemorrhagic RW1374 (0103:H2) and detection of a similar of serotype 0103:H2.";
                                                                                                                                                                                                                                                                             Schierack P., Tschaepe H., Wieler L.H., Schierack P., Tschaepe H., Wieler L.H., Schierack P., Tschaepe H., Wieler L.H., Vallence features in the enterchemorrhagic E. coli virulence features in the enterchemorrhagic E. coli
                                                                                                                                                                                                                                                                                                                                                                                                                        Rumer L., Jores J., Kirsch P., Cavignac Y., Zehmke K., Wieler "Dissemination of pheU and pheV located genomic islands among enteropathogenic (EPEC) and enterohemorrhagic (EHEC) E. coli consistent of the locus of enterposible role in the horizontal transfer of the locus of enterposible role in the horizontal transfer of the locus of enterposible role in the horizontal transfer of the locus of enterposible role in the horizontal transfer of the locus of enterposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (O103:H2) harboring a locus of enterocyte by intact insertion elements."; FEMS Microbiol. Lett. 204:75-79(2001).
                                                                                                                                                                                                             Distributed under the Creative
                                                                                                                                                                                                                         Copyrighted
                                                                                                                                                                                                                                                                                                                                                       STRAIN=RW1374;
                                                                                                                                                                                                                                                                                                                                                                                                             effacement
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=RW1374
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                                                                                                                                                                      Q5K5P9; 261-325.
                                                                                                                                                                                 AJ303141; CAI43867.1;
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72.7%;
82.1%;
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82.1%;
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                                           MW.
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Pred. No.
             Score 120;
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Commons Attribution-NoDerivs License
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.2e-06;
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                                           CRC64;
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RESULT 23
Q346799 RHOPA
ID Q346799;
AC Q346797;
DT 06-DEC-2
DT 07-FEB-2
DE Hypothet
GN ORFNames
OS Rhodopse
OC Bacteria
OC Bacteria
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CC Bradythi
OX NCBI Tax
RN NUCLEOTI
RC STRAIN=B
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Best Local
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06-DEC-2005,
07-FEB-2006,
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26-APR-2005,
07-FEB-2006,
                     STRAIN-BisB18
                                                                                                                       ORFNames=RPCDRAFT_4567;
Rhodopseudomonas palustris
                                                                                                                                                            Hypothetical
                                                                                                                                                                                                                                 Q34G79_RHOPA
Q34G79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003536; Tir_rcpt.
Pfam; PF07499; Tir_receptor_C; 1.
Pfam; PF03549; Tir_receptor_N; 1.
Pfam; PF07490; Tir_receptor_N; 1.
PRINTS; PR01370; TRNSINTIMINR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=15870341; DOI=10.1128/AEM.71.5.2511-2519.2005; Higgins J.A., Belt K.T., Karns J.S., Russell-Anelli J., Shelton D.R.; "tir- and stx-Positive Escherichia coli in Stream Waters in a Metropolitan Area.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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GO:0004872; F:receptor activity; IEA.
GO:0007155; P:cell adhesion; IEA.
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Pred. No.
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   (JGI-PGF);
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                                                                                                           Rhizobiales;
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                   InterPro;
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Query Match
Best Local Similarity
Matches 15; Conser
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Q7XWS7_ORYSA
Q7XWS7;
                                             Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
Enrartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
SEQUENCE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (NOV-2005) to the EMBL/GenBank/DDBJ databases -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequencing of the draft genome palustris BisB18.";
Submitted (OCT-2005) to the EMBI
                             NCBI_TaxID=39947
                                                                                                                         Name=OSJNBa0091C12.
                                                                                                                                         OSJNBa0091C12.5 protein.
                                                                                                                                                          07-FEB-2006,
                                                                                                                                                                        01-MAR-2004,
                                                                                                                                                                                           01-OCT-2003,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AALR01000001; EAP13698.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US DOE Joint Genome Institute (JGI-ORNL);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=BisB18
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary data.
                                                                                                                                                                                                                                                                                                                                            IGNLGNNVNGNHL-IPPAPPLPSQTD 26
                                                                                                                                                                                                                                                                                                                      VGSLGNLVGGNLANTPPAGPSPSDTD 1275
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1554 AA;
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                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                          entry version 14.
                                                                                                                                                                                             integrated into UniProtKB/TrEMBL.
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                                                                                                                                                                                                                                                                                                                                                                                                      40.3%;
57.7%;
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Feng Q., Zhang Y., Hao P., Wang S., Fu G., Huang Y., Li Y., Zhu J.,
Liu Y., Hu X., Jia P., Zhang Y., Zhao Q., Ying K., Yu S., Tang Y.,
Weng Q., Zhang L., Lu Y., Mu J., Lu Y., Zhang L.S., Yu Z., Fan D.,
Liu X., Lu T., Li C., Wu Y., Sun T., Lei H., Li T., Hu H., Guan J.,
Wu M., Zhang R., Zhou B., Chen Z., Chen L., Jin Z., Wang R., Yin H.,
Cai Z., Ren S., Lv G., Gu W., Zhu G., Tu Y., Jia J., Zhang Y.,
Chen J., Kang H., Chen X., Shao C., Sun Y., Hu Q., Zhang X., Zhang W.
Wang L., Ding C., Sheng H., Gu J., Chen S., Ni L., Zhu F., Chen W.,
Lan L., Lai Y., Cheng Z., Gu M., Jiang J., Li J., Hong G., Xue Y., GO; GO:0003779; F:actin binding; IEA.
GO; GO:0030036; P:actin cytoskeleton organization and biogenesis; IEA.
GO; GO:0016043; P:cell organization and biogenesis; IEA. Copyrighted by the UniProt Consortium, Distributed under the Creative Commons Gramene; Q7XWS7; -. EMBL; AL662989; Nature 420:316-320(2002). MEDLINE=22337377; PubMed=12447439; DOI=10.1038/nature01183; Sequence and analysis CAD39927.2; FH2_actin_bd of rice -: Genomic_DNA. chromosome see http://www.uniprot.org/terms
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Q4FX35;
30-AUG-2005, integrated ir 30-AUG-2005, sequence vers 07-FEB-2006, entry version Hypothetical protein. ORFNames=LMJ 1013;
Leishmania major strain F. Eukaryota; Euglenozoa; Ki
   STRAIN-Friedlin;
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EMBL; AP003700;
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Name=P0616D06.103; Synonyms=C011003 H02.130;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clade;
Ehrhartoideae; Oryzeae; Oryza.
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01-MAR-2003, sequence version
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GO:0004872; F:receptor activity;
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(GA3) genomic
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RESULT 27
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DT 01-JUN-2003, s
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RA Ivens A.C., Peacock C.S., Worthey E.A., Murphy L., Aggarwal G.,
RA Berriman M., Sisk E., Rajandream M.A., Adlem E., Aert R., Anupama A.,
RA Apostolou Z., Attipoe P., Bason N., Bauser C., Beck A., Beverley S.M.,
RA Apostolou Z., Attipoe P., Bason N., Bauser C.V., Collins M.,
RA Apostolou Z., Attipoe P., Bason N., Bauser C.V., Collins M.,
RA Cadag E., Ciarloni L., Clayton C., Coulson R.M.R., Cromin A.,
RA Cruz A.K., Davies R.M., De Gaudenzi J., Dobson D.E., Duesterhoeft A.,
RA Cruz A.K., Davies R.M., De Gaudenzi J., Dobson D.E., Duesterhoeft A.,
RA Fazelina G., Fosker N., Frasch A.C., Fraser A., Fuchs M., Gabel C.,
RA Goble A., Goffeau A., Harris D., Hertz-Fowler C., Hilbert H., Horn D.,
RA Huang Y., Klages S., Knights A., Kube M., Larke N., Litvin L.,
RA Lord A., Louie T., Marra M., Masuy D., Matthews K., Michaeli S.,
RA Mottram J.C., Mueller-Auer S., Munden H., Nelson S., Norbertczak H.,
RA Quilwer K., O'neil S., Pentony M., Pohl T.M., Price C., Purnelle B.,
RA Quail M.A., Rabbinowitsch E., Reinhardt R., Rieger M., Rinta J.,
RA Robben J., Rochein J., Schwartz D.C., Seeger K., Seyler A., Sharp S.,
RA Schaefer M., Schein J., Schwartz D.C., Seeger K., Seyler A., Sharp S.,
RA Schaefer M., Schein J., Schwartz D.C., Seeger K., Seyler A., Sharp S.,
RA Shin H., Sivam D., Squares R., Squares S., Tosato V., Vogt C.,
RA Zimmermann W., Smith D.F., Blackwell J.M., Stuart K.D., Barrell B.G.,
RA Zimmermann W., Smith D.F., Blackwell J.M., Stuart K.D., Barrell B.G.,
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Matches
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Bankier A.T., Dear P.H., Lehmann R., Baumgart
Abril J.F., Guigo R., Kumpf K., Tunggal B., Cc
Platzer M., Rosenthal A., Noegel A.A.;
"Sequence and analysis of chromosome 2 of Dict
Nature 418:79-85(2002).
PubMed=15875012; DOI=10.1038/nature03481; Eichinger L., Pachebat J.A., Gloeckner G., Sucgang R., Berriman M., Song J., Olsen R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dictyostelium discoideum
Eukaryota; Mycetozoa; Dic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Hypothetical protein). ORFNames=DDB0168607;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22092622; PubMed=12097910; DOI=10.1038/nature00847;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similar to Dictyostelium discoideum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/teDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=44689;
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hmann R., Baumgart C., Parra G.,
K., Tunggal B., Cox E.C., Quail M.A.,
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                                                               Tanaka Y., Shaulsky G., S
Cox E.C., Chisholm R.L.,
Kay R.R., Williams J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-AX4;
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24-MAY-2005,
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EMBL; AAFI01000018; EAL71429.1; -; Genomic_DNA.
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Pilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,
Feilcher K., Chen G., Saunders D., Sodergren E.J., Davis P.,
Kerhornou A., Nie X., Hall N., Anjard C., Hemphill L., Bason N.
Farbrother P., Desany B., Just E., Morio T., Rost R., Churcher
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279 AA; 3
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   of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
   social amoeba Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             social amoeba Dictyostelium discoideum.";
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50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dictyosteliida; Dictyostelium.
                                                                  Dear P.H., Noegel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Madera M., Konfortov
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 26;
3; Mismatches
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   discoideum.";
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RESULT 30
Q8HYB8 FELCA
ID Q8HYB8 F
AC Q8HYB8;
DT 01-MAR-2

ОВНУВВ FELCA ОВНУВВ;

PRELIMINARY;

PRT;

290

01-MAR-2003, integrated into UniProtKB/TrEMBL

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SOUTH THE COLOR OF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
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Best Local
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01-MAR-2003, sequen
07-FEB-2006, entry
Survival of motor n
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                   InterPro; IPR010304; SMN.
InterPro; IPR002999; Tudor.
Pfam; PF06003; SMN; 1.
                                                                                                                                                                                                                                                                                                                                                     HSSP; Q16637; IG5V.
G0; G0:0005737; C:cytoplasm; IEA.
G0; G0:0005534; C:nucleus; IEA.
G0; G0:0003723; F:RNA binding; IEA.
G0; G0:0003723; F:RNA processing;
G0; G0:0006397; P:mRNA processing;
G0; G0:000245; P:spliceosome assem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           He Q., Lowrie C., Fyfe J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBHYJ8_FELCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF503618; AAO14674.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mammalia; Eutheria; Laurasiatheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Felis silvestris catus (Cat).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AAFI01000066; EAL67262.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Distributed under the Creative Commons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 435:43-57(2005).
                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    preliminary data.
70
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                                             3 GNLGNNVNG-----NHLIPPAPPLPSQTDGAAR 30
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                                                                                                                    Similarity
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GNKSNNVKSKATSWNSFLPPPPPMPGAGLGPAK 102
                                                                                                                                                                                      116
116 AA;
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                                                                                             Conservative
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                                                                                                                                                                                           12339 MW;
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Pred. No.
                                                                                                                    Score 60.5;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                               assembly; IEA.
                                                                                                                                                                                           36F2831DE74E78D1 CRC64;
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Attribution-NoDerivs License
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RESULT
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   Query Match
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GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0005737; C:cytoplasm; IEA.
GO; GO:0005634; C:nucleus; IEA.
GO; GO:0003723; F:RNA binding; IEA.
GO; GO:0003723; F:RNA processing; IE
GO; GO:0006397; P:mRNA processing; IE
GO; GO:0000245; P:spliceosome assembl
InterPro; IPR010304; SMN.
InterPro; IPR010399; Tudor.
Pfam; PF06003; SMN; 1.
SMART; SM00333; TUDOR; 1.
PROSITE; PS50304; TUDOR; 1.
SEQUENCE 290 AA; 31326 MW; E4D15F
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01-OCT-2003,
07-FEB-2006,
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Q7TPJE RAT
                                                                                                                                       Ensembl;
                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE:
XU C.S., Li W.Q., Li Y.C., Yang K.J., Yan H.M., Chang C.
Ma H., Wang L., Wang S.F., Han H.P., Wang G.P., Chai L.G
Shi J.B., Rahman S., Wang Q.N., Zhang J.B.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia; Eutheria;
Muroidea; Muridae; M
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Felis silvestris catus (Cat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=SMN;
   Local Similarity
les 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175
                                                                                                                                AY321337; AAP86269.1; -; mRNA.
bl; ENSRNOG00000030738; Rattus norvegicus.
NCE 589 AA; 65537 MW; CE569D7608F2CA84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        016637;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lowrie
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rie C., Shelton
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                                  40.5%;
                                                                  36.7%;
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   <u>ب</u>
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                                  Score 60.5;
Pred. No. 6
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Pred. No. 3
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   10;
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                                                                                                                                    CRC64;
                                                              Length 589;
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   Indels
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Gaps
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J.Y.,
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Q55JM3 CRYNE Q55JM3; Q4-MAY-2005, 24-MAY-2005,

Hypothetical protein. ORFNames=CNBK3100;

neoformans

var.

neoformans B-3501A.

07-FEB-2006,

entry version

integrated into

UniProtKB/TrEMBL

PRELIMINARY;

PRT;

718

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RESULT 32

Q5X9X9 CRYNE
ID Q5X9X9

D7 15-FEB-2005, s
D7 15-FEB-2005, s
D7 15-FEB-2006, e
D8 Cytoplasm proto
GN CrearedlocusNa
OS Cryptococcus r
OC Tremellomyceti
OX NCBI TAXID=52(
RN (1)
CT STRAIN=JEC21;
RN Loftus B.J., i
RA Loftus B.J., i
RA Loftus B.J., i
RA Loftus D.J., i
RA Concolumn K., i
RA Loftus D.J., i
RA Schein J.B., i
RA Wye N.H., Kron
RA Fraser C.M., i
RA Schein J.B., i
RA Sc
RESULT 33
Q55JM3 CYNE
ID Q55JM3;
AC Q55JM3;
DT 24-MAY-2
DT 24-MAY-2
DT 24-MAY-2
DT 44-MAY-2
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DT 44-MAY-2
OR FUNDED
CREMANCS
OS CYPPLOCO
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Best Local Similarity
Matches 13; Conserv
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InterPro; IPRO01374; R3H_ss_bd.
InterPro; IPRO01374; R3H_ss_bd.
InterPro; IPRO00504; RNPI_RNA_bd.
Pfam; PF01424; R3H; 1.
Pfam; PF00076; RRM 1; 1.
SMART; SM00360; RRM; 1.
PROSITE: PSC1061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Loftus B.J., Fung E., Roncaglia P., Rowley D., Amedeo P., Bruno D., Vamathevan J., Miranda M., Anderson I.J., Fraser J.A., Allen J.E., Bosdet I.E., Brent M.R., Chiu R., Doering T.L., Donlin M.J., D'Souza C.A., Fox D.S., Grinberg V., Fu J., Fukushima M., Haas B.J., Huang J.C., Janbon G., Jones S.J.M., Koo H.L., Krzywinski M.I., Kwon-Chung K.J., Lengeler K.B., Maiti R., Marra M.A., Marra R.E., Mathewson C.A., Mitchell T.G., Pertea M., Riggs F.R., Salzberg S.L., Schein J.E., Shvartsbeyn A., Shin H., Shumway M., Specht C.A., Suh B.B., Tenney A., Utterback T.R., Wickes B.L., Wortman J.R., Wye N.H., Kronstad J.W., Lodge J.K., Heitman J., Davis R.W., Fraser C.M., Hyman R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cryptococcus neoformans (Filobasidiella neoformans).
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes;
Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytoplasm protein, putative OrderedLocusNames=CNK00330;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE017351; AAW46085.1; -; Genomic_DNA.
GO; GO:0003676; F:nucleic acid binding; IEA.
GO; GO:0000166; F:nucleotide binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Science 307:1321-1324(2005).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cryptococcus neoformans.";
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712 AA;
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ilarity 61.9%;
Conservative
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Best Local :
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                                                  Galagan J.E., Calvo S.E., Cuomo C., Ma L. J., Wortman J.R., Batzoglou S., Lee S.-I., Bastuerkmen M., Spevak C.C., Clutterbuck J., Kapitonov V., Jurka J., Scazzocchio C., Farman M., Butler J., Purcell S., Harris S., Braus G.H., Draht O., Busch S., D'Enfert C., Bouchier C., Goldman G.H., Bell-Pedersen D., Griffiths-Jones S., Doonan J.H., Yu J., Vienken K., Pain A., Freitag M., Selker E.U., Archer D.B., Penalva M.A., Oakley B.R., Momany M., Tanaka T., Archer D.B., Penalva M.A., Oakley B.R., Momany M., Tanaka T., Kumagai T., Asai K., Machida M., Nierman W.C., Denning D.W., Caddick M., Hynes M., Paoletti M., Pischer R., Miller B.L., Dyer P.S., Sachs M.S., Ogmani S.A., Birren B.W.;
"Sequencing of Aspergillus nidulans and comparative analysis with A. funigatus and A. oxyzae.";
Nature Albertin S. C., Candick M., Pischer R., Miller B.L., Dyer P.S., Tunigatus and A. oxyzae.";
                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein. ORFNames=AN4693.2;
                                                                                                                                                                                                                                                                                                                                                                                               26-APR-2005,
07-MAR-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Q5B437_EMENI
Q5B437;
                      Nature 438:1105-1115(2005).
                                                                                                                                                                                                                                          PubMed=16372000; DOI=10.1038/nature04341;
                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                      NCBI_TaxID=227321;
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
                                                                                                                                                                                                                                                                                                                                                 Aspergillus nidulans FGSC A4.
                                                                                                                                                                                                                                                                                                                                                                                                                           26-APR-2005,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical SEQUENCE 7:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS51061; R3H; 1. PROSITE; PS50102; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01424; R3H; 1.
Pfam; PF00076; RRM_1; 1.
SMART; SM00360; RRM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AAEY01000053; EAL17959.1; -;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Distributed under the Creative Commons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Cryptococcus neoformans serotype D sequencing. Submitted (JUL-2004) to the EMBL/GenBank/DDBJ da-i- CAUTION: The sequence shown here is derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fung E., Hyman R.W., Rowley D., Wickes B.L., Fu J., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=B-3501A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Heterobasidiomycetes; Tremellomycetidae; Tremellales; Tremellaceae; Filobasidiella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO; GO:0000166; F:nucleotide binding; InterPro; IPR012677; a b_plait nuc_bd. InterPro; IPR001374; R3H ss_bd. InterPro; IPR000504; RNPI_RNA_bd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=283643;
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EMENI
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               EMBL/GenBank/DDBJ whole
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718 AA; 7
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            genome
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Pred. No. 8
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            shotgun
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RA Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Ferriar C., Ferriar S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., J.H., Callasser K.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkilov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Merkilov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Singson M., Skupski M.P., Smith T.,
RA Shue B.C., Stapleton M., Strong R., Sun E.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Ye J., Yeh R.-F., Zaveri 
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Best Local
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-FEB-2006, entry vocG4636-PA (SD02991p)
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                                         Science
                                                                                                                        Zheng X.H., Zhong
Gibbs R.A., Myers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20196006;
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Ephydroidea; Drosophilidae; Drosophila.
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                                     .H., Zhong F.N., Zhong W., Zhou X., Zhu S
A., Myers E.W., Rubin G.M., Venter J.C.;
nome sequence of Drosophila melanogaster.
287:2185-2195(2000).
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Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R., Genzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K. Lewis S.E., Rubin G.M., Celniker S.; Submitted (OCT-2001) to the EMRI//~-~
FlyBase; FBgn0041781; SCAR.

GO; GO:0030037; P:actin filament reorganization during cell c.

GO; GO:0007413; P:axonal fasciculation; IMP.

GO; GO:00007413; P:cell projection biogenesis; IMP.

GO; GO:0010145; P:compound eye morphogenesis (sensu Endoptery.

GO; GO:0010866; P:cortical actin cytoskeleton organization an.

GO; GO:0008335; P:covarian ring canal stabilization; IMP.

GO; GO:0008330; P:regulation of cell shape; IMP.
                                                                                                                                                                              EMBL; AE003630; AAF53042.1; -; Genom EMBL; AY061579; AAL29177.1; -; mRNA. EMBL; AF247763; AAF74194.1; -; mRNA. FlyBase; FBgn0041781; SCAR.
                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome
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                                                                                                                                                                                                                                                                                                                                                                                            Submitted (MAR-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
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Celniker S., Carlson J., Wan K., Pf
Hoskins R., Stapleton M., Pacleb J.
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Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Ctanlaton M. Vamada C. Achburrack M. Calbart M.M. Rhidin G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted
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Kaminker J.S., Bergman C.M., Kronmiller
Patel S., Frise E., Wheeler D.A., Lewis
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MEDLINE=22426065; PubMed=12537568;
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"The transposable elements of the
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l. 3:RESEARCH0083.1-RESEARCH0083.
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05-UUL-2004, sequence version 1.
07-FBB-2006, entry version 12.
DNA internalization-related competence protein
DNA internalization-related competence protein
                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
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PubMed=15044751; DOI=10.1126/science.1094786;
Abrahamsen M.S., Templeton T.J., Enomoto S., J
Lancto C.A., Deng M., Liu C., Widmer G. Tzipc
Bankier A.T., Dear P.H., Konfortov B.A., Spri
Anantharaman V., Aravind L., Kapur V.;
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complexity with PFL0360c pfal
ORFNames=1MB.355, cgd6_2950;
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SMART; SM00246; WH2; 1.
PROSITE; PS51082; WH2;
SEQUENCE 613 AA; 670
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                                                  SEQUENCE
                                                                                               EMBL; AP007255; BAE52226.1;
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Distributed
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12:157-166(2005).
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RA Aggarwal G., Tran A.-N., Ghedin E., Worthey E.A., Delcher A.L.,

RA Aggarwal G., Tran A.-N., Ghedin E., Worthey E.A., Delcher A.L.,

RA Aggarwal G., Tran A.-N., Ghedin E., Carqueira G.C., Branche C.,

RA Aggarwal G., Westenberger S.J., Caler E., Cerqueira G.C., Branche C.,

RA Haas B., Anapuma A., Arner E., Aslund L., Attipoe P., Bontempi E.,

RA Bringaud F., Burton P., Cadag E., Campbell D.A., Carrington M.,

RA Crabtree J., Darban H., da Silveira J.F., de Jong P., Edwards K.,

RA Crabtree J., Darban H., da Silveira J.F., Ferella M., Frasch A.C.,

RA Englund P.T., Fazelina G., Feldblyum T., Ferella M., Frasch A.C.,

RA Gull K., Horn D., Hou L., Huang Y., Kindlund E., Klingbeil M.,

RA Gull K., Horn D., Hou L., Huang Y., Kindlund E., Klingbeil M.,

RA Kluge S., Koo H., Lacerda D., Levin M.J., Lorenzi H., Louie T.,

RA Machado C.R., McCulloch R., McKenna A., Mizuno Y., Mottram J.C.,

RA Nelson S., Ochaya S., Osoegawa K., Pai G., Parsons M., Pentony M.,

RA Pettersson U., Pop M., Ramirez J.L., Rinta J., Robertson L.,

RA Salzberg S.L., Sanchez D.O., Seyler A., Sharma R., Shetty J.,

**Simpson A.J., Sisk E., Tammi M.T., Tarleton R., Teixeira S.,
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144 ORYSA
QZQW44 ORYSA
QZQW44;
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24-JAN-2006, sequence versi
07-MAR-2006, entry version
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Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; BEP clauenthartoideae; Oryzeae; Oryza.
NCBI_TaxID=39947;
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Q4D3Y5;
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Buell C.R., Wing R.A., McCombie W.A., Ouyang S.;
Submitted (APR-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schizotrypanum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Euglenozoa;
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07-FEB-2006,
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Pred. No. 55;
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Search completed: August Job time : 305 secs
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Best Local Similarity
Matches 12; Conserv
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STRAIN=CL Brener;
E1-Sayed N., Bartholomeu D., Haas B.;
E1-Sayed N., Bartholomeu D., Haas B.;
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases.

-I- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                          EMBL; AAHK01001066; EAN87241.1; -; Genomic_DNA.
Hypothetical protein.
SEQUENCE 303 AA; 32793 MW; 93B64E99B4E47259
                                                                                                                                                                                                                                                                                                                                                                                                                               Hall N.;
"Comparative Genomics of Trypanosomatid Parasitic Protozoa.";
Science 0:0-0(2005).
[3]
NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CL Brener;

El-Sayed N.M.A., Myler P.J., Blandin G., Berriman M., Crabtree J.,
Aggarwal G., Caler E., Renauld H., Worthey E.A., Hertz-Fowler C.,
Ghedin E., Peacock C., Bartholomeu D.C., Haas B.J., Tran A.-N.,
Wortman J.R., Alsmark U.C.M., Angiuoli S., Anupama A., Badger J.,
Baringaud F., Cadag E., Carlton J.M., Cerqueira G.C., Creasy T.,
Delcher A.L., Djikeng A., Embley T.M., Hauser C., Ivens A.C.,
Kummerfeld S.K., Pereira-Leal J.B., Nilsson D., Peterson J.,
Salzberg S.L., Shallom J., Silva J.C., Sundaram J., Westenberger S.,
White O., Melville S.E., Donelson J.E., Andersson B., Stuart K.D.,
                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Van Aken S., Vogt C., Ward P.N., Wickstead B., Wortman J., White O., Fraser C.M., Stuart K.D., Andersson B.; "The Genome Sequence of Trypanosoma cruzi, Etiologic Agent of Chagas' Disease.";
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66.7%; Pred. No. ...
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              2006, 21:46:41
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Sequence:
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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1: /EMC Celerra SIDS3/ptodata/2/iaa/5 COMB.pep:*
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3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7 COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
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IS-09-270-767-60141
IS-09-270-767-44686
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IS-09-252-991A-19252
IS-09-252-991A-28228
IS-09-252-991A-28228
IS-09-253-991A-28228
IS-09-377-2858-20
IS-09-189-035-1
IS-09-189-035-1
IS-09-189-035-1
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S-09-270-767-61121
S-10-104-047-2072
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S-09-080-897-4
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30386, A
30327, A
40686, A
106, App
19252, A
106, App
19252, A
202, Appl
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23127, A
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US-09-270-767-60585
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US-09-895-674A-1
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US-08-468-996-10
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US-08-931-820-3
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US-09-500-811-20
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US-09-949-016-8569
Sequence 1, Appli Sequence 2, Appli Sequence 45089, A Sequence 110, Appli Sequence 110, Appli Sequence 110, Appli Sequence 110, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 20, Appli Sequence 3112, Appli Sequence 31164, Appli Sequence 31164, Appli Sequence 31164, Appli Sequence 3117, Appli Sequence 3117, Appli Sequence 62, Appli Sequence 62, Appli Sequence 62, Appli Sequence 63, Appli Sequence 11016, Appli Sequence 3101, Appli Sequence 
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US-09-270-767-41663
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT FILING DATE: 1999-03-17
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 41663
LENGTH: 268
TYPE: PRT
ORGANISM: Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 41663, Application US/09270767 Patent No. 6703491
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                                                                                                             APPLICATION NUMBER: US/01
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM CC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: MCCONNELL,
TITLE OF INVENTION: PO
TITLE OF INVENTION: DO
TITLE OF INVENTION: UI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                           NAME: MISTOCK, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 111
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                         CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 48.1 nes 13; Conservative
                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                               STREET:
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              TELEPHONE: (212) 790~9090
TELEFAX: (212) 869-8864/9741
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66141 PENNIE
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                                                                                                                                                                                                                                                                                                            USA
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POLYPEPTICES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
USING SAME
                                                                                                                                                                     US/08/630,915A
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                                                                1101-174
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                                                  FEATURE:
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; NAME/KEY: Other
; OTHER INFORMATION: Biotinylated N-terminal
US-08-630-915A-67
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Patent No. 6709821
GENERAL INFORMATION:
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                                                                                                                                                                             TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 67: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
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TOPOLOGY: un
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COMPUTER REALDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING RESENTING Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/630,915
ETLING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
OTHER INFORMATION: Biotinylated N-terminal SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: SPARKS, Andrew B.
HOFFMAN, No. 6709821h
                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 GNNVNGNHLIPPAPPLPSQTDG 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1155 Avenue of the Americas
                                        NAME/KEY:
                                                                                                     TOPOLOGY: unknown
                                                                                                                                         TYPE: amino acid
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                                                                                                                                                            LENGTH: 22 amino acids
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                                        Other
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50.0%;
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Pred. No. 1
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   RESULT 6
US-08-653-648A-14
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US-09-489-039A-13282
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CURRENT FILING DATE: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 794
SEQ ID NO 794
TYPE: PRT
ORGANISM: Eucalyptus grandis
                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS:
SEQ ID NO 13282
LENGTH: 474
                                                                                                                                            Query Match
Best Local Similarity
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APPLICANT: Gary Bro
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No. 661083
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Best Local (
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: McGrath, Annette
APPLICANT: Glenn, Matthew
TITLE OF INVENTION: Compositions and Methods for the
TITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021CID
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                      ORGANISM: Klebsiella pneumoniae
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                                                                                            11 GNHLIPPAPPLPSQTDGAAR 30
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                                                                 GNHLLRPAPGLPMAKQAPAR 100
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38.5%;
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Pred. No. 47;
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Pred. No. 1
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                                                            RESULT 8
US-09-252-991A-26444
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; LENGTH: 674
; TYPE: PRT
              Sequence 26444, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
APPLICANT: Marc J.
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US-08-653-648A-14
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CURRENT APPLICATION NUMBER: US/08/653,648A
CURRENT FILING DATE: 1995-05-24
PRIOR APPLICATION NUMBER: GB 9510759.5
PRIOR FILING DATE: 1995-05-26
PRIOR APPLICATION NUMBER: GB 9605656.9
PRIOR APPLICATION NUMBER: GB 9513882.2
PRIOR FILING DATE: 1996-03-18
PRIOR FILING DATE: 1996-07-07
PRIOR FILING DATE: 1995-07-07
PRIOR FILING DATE: 1995-07-07
PRIOR APPLICATION NUMBER: GB 9517316.7
PRIOR APPLICATION NUMBER: GB 9517316.7
PRIOR APPLICATION NUMBER: GB 9517316.7
PRIOR PILING DATE: 1995-08-24
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.0
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Best Local Similarity
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Patent No. 6610828
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CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 09/564,418
PRIOR FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 63
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APPLICANT: Jepson, Ian
APPLICANT: Martinez, Alberto
APPLICANT: Greenland, Andrew James
TITLE OF INVENTION: A GENE SWITCH
FILE REFERENCE: 1392/4/3
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115 VGNLINGVNPNOTLIPPLPSIIQNT 139
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Similarity 52.0%;
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Pred. No. 80;
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Pred. No. 80;
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Rubenfield et al

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LENGTH: 618
TYPE: PRT
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LENGTH: 631
SEQ ID NO 22421
                                                                   APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1998-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
                 PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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ORGANISM: Pseudomonas aeruginosa
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48.0%;
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PRIOR FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 30386

LENGTH: 623

TYPE: DDT
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                                                             US-09-252-991A-30227
                                                                                                                                                                                   APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO A
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTI
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION UNBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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US-09-252-991A-30227
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US-09-252-991A-30386
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                                                                                         PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30227
LENGTH: 2736
TYPE: PRT
 Matches
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APPLICANT: Marc J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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GENERAL INFORMATION:
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                 Best
                              Query Match
                                                                                                                                                                                                                                                                                                                               Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                            Sequence 30227,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 623
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 211
TYPE: PRT
ORGANISM: Candida albicans
                                                                            ORGANISM: Pseudomonas aeruginosa
                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 NGNHLIPPAPPLPSQTDG
                                                                                                                                                                                                                                                                                                                                                                                                                              28 SGCHGLPPAPPAPSAAVG
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              h 32.7%; Score 54; DB 2;
Similarity 44.0%; Pred. No. 5.8e+02;
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 Conservative
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                                                                                                                                                                                                                                                                                                                                              Application US/09252991A
                                                                                                                                                                                                                                                    ON: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS 107196.136
                                                                                                                                                                                umbER: US 60/074,788
1998-02-18
                                                                                                                                                                                                                                                                                 Rubenfield et al.

NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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50.0%;
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Pred. No. 1.1e+02;
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Pred. No.
Mismatches
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                              Length 2736;
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PIGQTTADANGNWSFTPSTPLPDGT 583

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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION UNMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
UNMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 44686
LENGTH: 253
TYPE: PRT
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US-08-311-731A-106
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US-09-270-767-60141
                                                                                                                                                                             Sequence 106, Application US/08311731A Patent No. 6583266 GENERAL INFORMATION:
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APPLICANT: Homburger et al.
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 60141
LENGTH: 121
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Patent No. 6703491
GENERAL INFORMATION:
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Best Local Similarity
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                                                                 APPLICANT: MAO, JEN-I
TITLE OF INVENTION: N
TITLE OF INVENTION: D
TITLE OF INVENTION: D
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
OTHER INFORMATION: Xaa means any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Drosophila melanogaster
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
WOLF, GREENFIELD & SACKS, P.C.
STREET: 600 ATLANTIC AVENUE
                                                                                                                                          APPLICANT: SMITH, APPLICANT: MAO, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                          175 PKSSRRSRISGGLVMPPMPPVPPMIVGQGDGA 206
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                                                                             NUCLEIC ACID AND AMINO ACID SEQUENCES
RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR DIAGNOSTICS AND THERAPEUTICS
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 253;
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US-09-252-991A-19252
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US-09-252-991A-19252
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                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 19252
LENGTH: 832
                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6551795 GENERAL INFORMATION:
                                                                                    Best
                                                                  Matches
                                                                                               Query Match
                                                                                                                                                                                                                                                                  APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19252,
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Best Local Similarity
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NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C004
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/720-3500
TELEPAX: 617/720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                     TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 530
                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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406 PALGIRHRARGRHILPPAPRRP 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 PPAAPLPGHTDGTS 196
                                                                  10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16 PPAPPLPSQTDGAA 29
                      1 PIGNLGNNVNGNHLIPPAPPLP 22
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                                                                 Conservative
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                                                                                 Score 53;
Pred. No. 2
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Pred. No. 1.4e+02;
                                                                 Mismatches
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                                                                                                  DB 2;
                                                                                                Length 832;
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                                                                 Indels
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RESULT 17 US-09-252-991A-28228

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RESULT 18
US-09-377-285B-20
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RESULT 19
US-10-192-381-20
; Sequence 20, A
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Best Local Similarity
Thes 9; Conserve
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LENGTH: 219
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                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 20
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                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BENEKEN, Jutta
APPLICANT: LANAHAN, Anthony
TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS AMENDED)
FILE REFERENCE: JUUI580-4
CURRENT APPLICATION NUMBER: US/09/377,285B
CURRENT FILING DATE: 1999-08-18
PRIOR APPLICATION NUMBER: US 60/138,426
PRIOR FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US 60/138,493
PRIOR FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US 60/138,494
PRIOR FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US 60/138,494
PRIOR PILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US 60/097,334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE APPLICANT: WORLEY, Paul APPLICANT: TU, Jian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn ver
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                      LENGTH: 366
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Local Similarity 50.0%;
les 9; Conservative
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                                                                                                                                          16 PPAPPLPSQTD 26
                                                                                                     PPAPPLPSSLD 242
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LEAHY, Daniel
    Application US/10192381
                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                    31.5%;
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Pred. No.
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Pred. No. 1.1e+02;
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63;
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APPLICANT: BENEKEN, JUTTA
APPLICANT: LANAHAN, Anthony
TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING HOMER 1b PROTEIN (AS
TITLE OF INVENTION: AMENDED)
FILE REFERENCE: JHHI1580-4
CURRENT APPLICATION NUMBER: US/10/192,381
CURRENT FILING DATE: 1992-08-18
PRIOR APPLICATION NUMBER: US 60/377,285
PRIOR APPLICATION NUMBER: US 60/138,426
PRIOR APPLICATION NUMBER: US 60/138,426
PRIOR FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US 60/138,493
PRIOR APPLICATION NUMBER: US 60/138,494
PRIOR APPLICATION NUMBER: US 60/138,494
PRIOR APPLICATION NUMBER: US 60/138,494
PRIOR FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US 60/138,494
PRIOR FILING DATE: 1999-06-10
PRIOR FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US 60/138,494
PRIOR FILING DATE: 1999-06-10
PRIOR FILING DATE: 1999-06-10
PRIOR APPLICATION NUMBER: US 60/097,334
PRIOR FILING DATE: 1998-08-18

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US-09-189-035-1
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                                                                                                                                                                                 US-09-189-035-1
                                                                                                                                                                                                                                                                                         SOFTWARE: PERL Program
SEQ ID NO 1
LENGTH: 476
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Patent No. 6020165
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GENERAL INFORMATIO
                                                                                       Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/189,035
CURRENT FILING DATE: 1998-11-10
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yue, Henry
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: CYTOKINE SIGNAL REGULATORS
FILE REFERENCE: PF-0638 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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OTHER INFORMATION: 2280326
                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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Local Similarity 81.8%;
es 9; Conservation
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342 PPAPPLPSSLD 352
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                                          PPAPPLPSQTD 26
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LEAHY, Daniel
                                                                                       Conservative
                                                                                                               31.5%;
                                                                                       0; Mismatches
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Pred. No. 1.1e+02;
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Pred. No. 1.5e+02;
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Sequence 1, Application US/09382086
Patent No. 6201106
GENERAL INFORMATION:
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Guegler, Karl J.
APPLICANT: Bughn, Mariah R.
FILE OF INVENTION: CYTOKINE SIGNAL REGULATORS
FILE REFERENCE: PF-0638 US
CURRENT APPLICATION NUMBER: US/09/382,086
CURRENT APPLICATION NUMBER: US/09/382,086
CURRENT FILING DATE: 1999-08-24
EARLIER APPLICATION NUMBER: 09/189,035
EARLIER FILING DATE: 1998-11-10
NUMBER OF SEO ID NOS: 6
SOPTWARE: PERL PROGram
SEO ID NO 1
I-ENGTH: 476
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US-09-270-767-61121
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APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
Sequence 61121, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
SEQ ID NO 23187
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Best Local
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Best Local S
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CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: -
                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 690
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9; Conserva
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Pred. No. 2.2e+02;
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Pred. No. 1.5e+02;
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Query Match
Best Local Similarity
Marches 8; Conserve
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US-09-198-452A-63
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                                                                                                                   US-09-198-452A-63
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                                                                                                                                                NUMBER OF SEQ I
SEQ ID NO 63
LENGTH: 644
TYPE: PRT
                                                                                                                                                                                                TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, frag
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis,
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2072
LENGTH: 509
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CURRENT FILING DATE: 1999-03-17
NUMBER OF SEO ID NOS: 62517
SOFTWARE: PATENTIN Ver. 2.0
SEO ID NO 61121
LENGTH: 55
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6943241
GENERAL INFORMATION:
                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                             Sequence 63, Application US/09198452A Patent No. 6559294
                                                  Matches
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Matches 1
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TITLE OF INVENTION: No. 6943241e1 full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                               ORGANISM: Chlamydia pneumoniae
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12 NHLIPPAPPLPSQTDGAA 29 : | | | | | | : | |:
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                                                  Conservative
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                                                                30.9%; Score 51; DB 2; 50.0%; Pred. No. 2.8e+02;
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Pred. No.
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Pred. No.
                                                 Mismatches
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                                                                                   Length 644;
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                                                                                                                                                                                        Sequence 1, Application US/08899595
Patent No. 6111072
                                                                                                                                                                                                                                                                                                                                                                       Query Match 30.9%; Score 51; DB 1; Best Local Similarity 44.4%; Pred. No. 5.8e+02; Matches 8; Conservative 5; Mismatches 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (650) 343-434;
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
                                                                                               APPLICANT: Narumiya, Shuh
APPLICANT: Takahashi, No. 6111072uaki
TITLE OF INVENTION: RHO TARGET PROTEIN HUMAN MDIA AND GENE
TITLE OF INVENTION: ENCODING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UW97-001
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/080,897 FILING DATE:
                                                                 NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Morrow, Jan E.
APPLICANT: Welcsh, Piri L.
APPLICANT: Leon, Pedro E.
TITLE OF INVENTION: Modulators of Actin
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
       STREET: 3000 K ST
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1255 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
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                             ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W.,
                                                                                                                                                                                                                                                                                                      564 SVSSSAAVPPAPPLPGDS 581
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5. 5985574
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T: 75 DENISE DRIVE
HILLSBOROUGH
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                                 Suite 500
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US-09-323-735-4
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APPLICANT: King, I
APPLICANT: Lynch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEX: 904136
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino aci
                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/323,735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 26-AUG-1996
PRIOR APPLICATION DATE: JP 9-90170
PRILING DATE: 25-MAR-1997
ATTORNBY/AGENT IMPORMATION:
NAME: CFORMAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,595
FILING DATE: 24-JUL-1997
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                    ZIP: 94010
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Modulators of Actin NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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Local Similarity 44.4%;
es 8; Conservarino
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                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
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Welcsh, Piri L.
Leon, Pedro E.
                                                                                                                                                                                                              USA
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(202) 672-5399
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Pred. No. 5.8e+02;
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Requence 2, Application US/09692945
Retent No. 6797695
GENERAL INFORMATION:
APPLICANT: Chiron Corporation
APPLICANT: Kyoto University
APPLICANT: Kavanaugh, Michael W.
TITLE OF INVENTION: HUMAN FGF-20 GENE AND GENE EXP
TITLE OF INVENTION: HUMAN FGF-20 GENE AND GENE EXP
TITLE REFERENCE: 60219-6/16770.001
CURRENT APPLICATION NUMBER: US/09/692,945
CURRENT FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 212
Type: PAT
ORGANISM: Rattus norvegicus
US-09-692-945-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster

FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 60585

LENGTH: 78

TYPE: PRT

ORGANISM: Drosophila melanogaster

US-09-270-767-60585
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US-09-692-945-2
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US-09-270-767-60585
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Best Local Similarity
Marches 8; Conserve
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Best Local Similarity
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TELEPAS: (650) 343-4342
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sir
TOPOLOGY: linear
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linear
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Pred. No. 31;
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fortala, Andrzej
APPLICANT: KO, Frank
ITILE OF INVENTION: Collagen and Collagen-like Peptide Containing Polymeric
ITILE OF INVENTION: Matrices
FILE REFERENCE: DRE-0032
CURRENT APPLICATION NUMBER: US/09/895,674A
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: PCT/US01/
PRIOR FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: 60/ 214,034
PRIOR FILING DATE: 2000-06-23
NUMBER OF SEQ ID NOS: 1
SEQ ID NO 1
SEQ ID NO 1
LENGTH: 234
TYPE: PRI
TYPE: 
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                                                                                                                                                                                                                                                   ; ORGANISM: Drosophila melanogaster US-09-270-767-45089
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US-09-270-767-45089
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US-09-895-674A-1
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                                                                                                                                                                                                                                                                                                     Sequence 45089, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 45089
LENGTH: 259
TYPE: PRT
                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                             Matches
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Best Local
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match 30.6%;
Local Similarity 46.2%;
201
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                                              NLGNNVNGNHLIPPAPPLPSQTDGAA 29
NLSMHGNGGEL-PAATPLPAVSDEAA 225
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                                                                                                                      30.6%; ilarity 50.0%; Conservative
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                                                                                                                      Score 50.5; DB 2;
Pred. No. 1.2e+02;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50.5; DB:
Pred. No. 1e+02;
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Pred. No. 93;
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7:
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RESULT 33 US-09-623-497-1

Application US/09623497

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                                                                                                                                                                                           RESULT 35
US-08-468-996-10
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; TYPE: PRT
; ORGANIZM: Human cytomegalovirus
US-10-332-795-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-332-795-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: The University Court of the University of Glasgow APPLICANT: Clements, John Barklie
APPLICANT: MacLean, Alasdair Roderick
TITLE OF INVENTION: HERPES ZINC FINGER MOTIFS
FILE REFERENCE: 9013-51
                                                                                                                                                    Sequence 10, Application US/08468996 Patent No. 6645504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
                                                                                                                                  GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: MACKAY, IAN
TITLE OF INVENTION: METHOD FOR THE DIAGNOSIS OF RHEUMATOID ARTHRITIS
FILE REFERENCE: 017227/0167
CURRENT APPLICATION NUMBER: US/09/623,497
CURRENT FILLING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: PCT/AU98/00176
PRIOR PRIOR PLING DATE: 1998-03-18
PRIOR FILING DATE: 1998-03-18
PRIOR APPLICATION NUMBER: AN PO5712/97
PRIOR PLING DATE: 1997-03-19
NUMBER OF SEQ ID NOS: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
              APPLICANT: Weiner, Howard
APPLICANT: Miller, Ariel
APPLICANT: Zheng, Zhengi
APPLICANT: Zheng, Zhengi
APPLICANT: Ahmad, Al-Sabbagh
TITLE OF INVENTION: BYSTANDER SUPPRESSION OF TYPE 1 DIABETES BY ORAL ADMINISTRATION
TITLE OF INVENTION: GLUCAGON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/332,795
CURRENT FILING DATE: 2003-01-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: COOK,
APPLICANT: ROWLE
APPLICANT: MACKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: GB 0016890.6 PRIOR FILING DATE: 2000-07-11
FILE REFERENCE: 1010/16959-US3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH: 347
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                                                                                                                                                                                                                                                                         692 SANGNHSTTATQQQQPPPPPPPPPPPQEDD 721
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Pred. No. 1.6e+02;
2; Mismatches 9
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; SEQ ID NO 10
; LENGTH: 1017
; TYPE: PRT
; ORCANISM: Homo sapiens
US-08-468-996-10
US-08-931-820-3
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CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: US 07/843,752
PRIOR FILING DATE: 1992-02-28
PRIOR APPLICATION NUMBER: US 07/460,852
PRIOR FILING DATE: 1990-02-21
PRIOR PPLICATION NUMBER: US 07/596,936
PRIOR APPLICATION NUMBER: US 07/065,734
PRIOR APPLICATION NUMBER: US 07/065,734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application Patent No. 6010863
GENERAL INFORMATION:
APPLICANT:
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                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1060 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1989-07-14
PRIOR APPLICATION NUMBER: US 07/607,826
PRIOR FILING DATE: 1990-10-31
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PRIOR APPLICATION NUMBER: US 07/551,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 07/454,486 PRIOR FILING DATE: 1989-12-20
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                                      MOLECULE TYPE: protein HYPOTHETICAL: NO ORIGINAL SOURCE: ORGANISM: Homo sapier
                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 96202596.1
                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NUMBER OF SEQUENCES:
                     TISSUE TYPE:
                                                                                                                                        STRANDEDNESS:
                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                      TOPOLOGY:
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12; Conserv
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                                                                                                                                                                                1060 amino acids
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                                                                                                                      linear
                   Homo sapiens
E: Collagen type II
                                                                                                                                        single
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Pred. No. 5.3e+02;
2; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                        Version #1.25 (EPO)
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1;

Query Match

30.6%;

Score 50.5;

DB 2;

Length 1060;

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US-09-010-999-1
US-09-010-999-1
; Sequence 1, Application US/09010999
; Patent No. 6132976
; Patent INFORMATION:
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                                                                                RESULT 38
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                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 12; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US/08/187,319
FILING DATE: 21-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: GOGOTIS, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 4305/08701
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEPAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/963,825
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: but
STREET: New York
CITY: New York
TISA
                                                                                                                                                                                                                                                                                     IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1418 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                836 VGPPGSNGNPG---PPGPPGPSGKDG 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       724 VGPPGSNGNPG---PPGPPGPSGKDG 746
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5. 6110689
                                                                                                                                                                2 IGNLGNNVNGNHLIPPAPPLPSOTDG 27
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                                                                                                                                                                                                                                                                                                                                                                                          amino acid
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805 Third Avenue
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Conservative
                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                         linear
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                                                                                                                                                                                                                                                                                                                                                       protein
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in Body Fluids, A Test Kit and Means for Carrying Out the
Method and Use of the Method to Diagnose the Presence of
Disorders Associated with the Metabolism of
                                                                                                                                                                                                                 30.6%; Score 50.5; DB 2; 46.2%; Pred. No. 7.6e+02;
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                                                                                                                                                                                                2; Mismatches
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                                                                                                                                                                                                                                Length 1418;
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RESULT 39
US-09-500-811-20
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Best Local Similarity
Watches 12; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Human Type II Collagen US-09-010-999-1
                                                                                                                                                                                                                              Sequence 20, Applicati
Patent No. 6323314
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/448,501
FILING DATE: 17-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,123
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 032931/021:
TELECOMMUNICATION INFORMATION:
                                                                                                             APPLICANT: Qvist, Per
APPLICANT: Bonde, Martin
TITLE OF INVENTION: A Meth
TITLE OF INVENTION: in Bod
TITLE OF INVENTION: bisord
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INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hollander, Anthony P.

APPLICANT: Billinghurst, R. C.

TITLE OF INVENTION: IMMUNOASSAYS FOR THE MEASUREMENT OF
TITLE OF INVENTION: COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE
NUMBER OF SEQUENCES: 16
                                                                        CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1418 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 3000
CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 22-JAN-1998 CLASSIFICATION: 4335
                                    STREET:
                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (202) 672-53
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Foley & Lardner
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                                                                                                                                                                                                                                                                                                                                                                                                          2 IGNLGNNVNGNHLIPPAPPLPSQTDG 27
                    New York
New York
                                                                                                                                                                                                                                                                      Application US/09500811
                                    805 Third Avenue
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                                                        Darby
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                                                      & Darby PC
                                                                                                             A Method for Assaying Collagen Fragments in Body Fluids, A Test Kit and Means for Carrying Out the Method and Use of the Method to Diagnose the Presence of Disorders Associated with the Metabolism of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      us/09/010,999
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US-09-570-573-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 20, App. -- No. 6342361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 30.6%; Score 50.5; DB 2; Best Local Similarity 46.2%; Pred. No. 7.6e+02; Matches 12; Conservative 2; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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PILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: GOGOTIS, Adda C

REGISTRATION NUMBER: 29,714

REFERENCE/DOCKET NUMBER: 4305

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICATION NUMBER: UPFILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
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STREET: New York
CITY: New York
TTATE: New York
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Qvist, Per APPLICANT: Bonde, Martin APPLICANT: Bonde, Martin TITLE OF INVENTION: A Method for Assaying Collagen Fragments TITLE OF INVENTION: in Body Fluids, A Test Kit and Means for Carrying Out the TITLE OF INVENTION: Method and Use of the Method to Diagnose the Presence of NUMBER OF INVENTION: Disorders Associated with the Metabolism of NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,811
                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
CLONE: COLLAGEN -ALPHA 1 (II)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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TELEPHONE: 212-753-6237
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                                                                                                                                                                                                                                                                                                               E: Darby & Darby PC
805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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    08/187,319
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                                                                                   US/09/570,573
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; CLONE: COLLAGEN -ALPHA 1 (II)
US-09-570-573-20
Job time : 52 secs
             Search completed: August 1, 2006, 21:48:16
                                                                                                                              Matches
                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212-753-6237
TELEX: 236687
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                           MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                           NAME: Gogoris, Adda C
REGISTRATION NUMBER: 29,714
REFERENCE/DOCKET NUMBER: 43
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
TELEPAX: 212-753-6237
                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1418 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                               836 VGPPGSNGNPG---PPGPPGPSGKDG 858
                                                                                                                            12;
                                                                                            2 IGNLGNNVNGNHLIPPAPPLPSQTDG 27
                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                            30.6%;
ilarity 46.2%;
Conservative
                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                             linear
                                                                                                                            2
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                                                                                                                            Score 50.5; DB 2;
Pred. No. 7.6e+02;
2; Mismatches 9;
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                                                                                                                                                           Length 1418;
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 100 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                     Score
       веq
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length: 2000000000
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Match
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165
1 PIGNLGNNVNGNHLIPPAPPLPSQTDGAAR
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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       Copyright
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     558

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  US-11-134-563-12
US-11-134-7963-1184318
US-10-437-963-177853
US-11-097-143-9273
US-10-264-049-2829
US-10-264-049-2829
US-10-264-049-2829
US-10-312-352-13
US-10-745-237-260
US-10-032-585-7691
US-10-415-656-2
US-09-835-232-2
US-10-308-485-2
US-10-308-485-2
US-10-308-485-2
US-10-424-599-249972
US-10-856-832-157
US-10-856-832-157
US-10-856-499-794
US-10-856-499-794
US-10-856-493-21572
US-10-369-493-21572
US-10-369-493-21572
US-10-424-599-29211
US-10-424-599-29950
                                                                                                                                                                                                                                                                                                                                                                                                                                             SUMMARIES
Sequence 12, Appl Sequence 184318, Sequence 18733, Ap Sequence 187133, Sequence 187133, Sequence 187133, Sequence 187133, Sequence 116, App Sequence 260, Appli Sequence 260, Appli Sequence 2, Appli Sequence 112409, Sequence 1062, Appli Sequence 107, Appli Sequence 107, Appli Sequence 167, Appli Sequence 157, Appli Sequence 249972, Sequence 21572, Appli Sequence 27, Ap
                                                                                                                                                                                                                                                                                                                                                                                                  Description
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       US-11-150-845-47
US-10-666-606A-12
US-10-425-115-21796
US-10-425-115-24273
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US-10-425-115-24273
US-10-108-260-4737
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US-10-425-114-72250
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RESULT 3
US-10-437-963-184318
; Sequence 184318, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
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TYPE: PRT
; ORGANISM: Escherichia coli 0157:H7
US-11-052-554A-20
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TYPE: PRT
; ORGANISM: Escherichia coli
US-11-134-563-12
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Best Local S
Matches 23
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APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION UNMEER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.3 SEQ ID NO 20
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Publication No. US20050288866A1
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Best Local
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APPLICANT: Campellone, Kenneth G.
APPLICANT: Campellone, Kenneth G.
TITLE OF INVENTION: ESPETU NUCLEIC ACIDS AND PROTEINS AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 07917-280001
CURRENT APPLICATION NUMBER: US/11/134,563
CURRENT APPLICATION NUMBER: US/11/134,563
CURRENT FILING DATE: 2005-05-20
PRIOR APPLICATION NUMBER: US 60/573,600
PRIOR APPLICATION NUMBER: US 60/573,600
PRIOR FILING DATE: 2004-05-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR APPLICATION NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-02-06
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Pred. No. 2.7e-06;
2; Mismatches 3
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CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 184318
LENGTH: 986
TYPE: PRT
                                                                                  Query Match
Best Local :
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SEQ ID NO 177853
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                                                                    Matches
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APPLICANT:
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APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
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                                                                                                                                                                   NAME/KEY: unsure
LOCATION: (1)..(173)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Oryza sativa
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                                                                                Match 37.0%;
Local Similarity 68.8%;
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144 NGXHLGPPAPPPPGRT 159
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Kovalic, David I
Zhou, Yihua
Cao, Yongwei
                       NGNHLIPPAPPLPSQT 25
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Wei
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Barbazuk, Brad
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                                                                  Conservative
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                                                                                  Score 61; DB 4; Length 173; Pred. No. 21;
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RESULT 5 US-11-097-143-9273

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                                                                                                              ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_139994C.1.pep
US-10-424-599-187133
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SEQ ID NO 187133
LENGTH: 146
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SOFTWARE: FastSEQ for Windo
SEQ ID NO 9273
LENGTH: 613
                                                                  Query Match
Best Local Similarity
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                                                       Matches
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APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: 10/10/424,599
CURRENT FILING DATE: 2003-04-28
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Best Local Similarity
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
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CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: DETECTION KIT, SUCH AS TITLE OF INVENTION: ARRAYS, FOR DETECTING TITLE OF INVENTION: DROSOPHILA GENES.
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PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
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                                                                                                                                                                           TYPE: PRT
ORGANISM: Glycine max
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1 PIGNLGNNVNGNHLIPPAPPLPSQ 24
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. US20050208558A1
                                                     Conservative
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••
                                                                    Score 59; DB 4; Length 146; Pred. No. 30;
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Pred. No. 1e+02;
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US-10-714-887-116
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RESULT 8
US-10-264-049-2829
                     Sequence 2829, Application US/10264049
Publication No. US20040005579A1
GENERAL INFORMATION:
APPLICANT: Birse et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PA133P1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 430

SOFTWARE: PatentIn version 3.2

SEQ ID NO 116

LENGTH: 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SHERMAN, Bradley K
TITLE OF INVENTION: PLANT TRANSCRIPTIONAL REGULATORS OF DROUGHT STRESS
FILE REFERENCE: MBIO058-CIP
CURRENT APPLICATION NUMBER: US/10/714,887
CURRENT FILING DATE: 2003-11-13
PRIOR APPLICATION NUMBER: 10/412,699
PRIOR PILING DATE: 2003-04-10
PRIOR PILING DATE: 2003-04-10
PRIOR FILING DATE: 2000-02-17
PRIOR FILING DATE: 2000-02-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 60/125,814
PRIOR FILING DATE: 1999-03-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/135,134
PRIOR FILING DATE: 1999-05-20
PRIOR APPLICATION NUMBER: 09/394,519
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 09/533,392
PRIOR FILING DATE: 2000-03-22
CURRENT APPLICATION NUMBER: US/10/264,049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/713,994
PRIOR FILING DATE: 2000-11-16
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PRIOR APPLICATION NUMBER: 09/532,591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/533,392
PRIOR FILING DATE: 2000-03-22
PRIOR APPLICATION NUMBER: 09/533,029
                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: G3683 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT Oryza sativa (japonica cultivar-group)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/533,030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 2000-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION:
                                                                                                                                                                                                                                                                                    3 GNLGNNVNGNHLIPPAPPLPSQTDGA 28
                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                 GGGGGGMNGRHMSPPTPPAAAEESKA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REUBER, T. Lynne
PINEDA, Omaira
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIECHMANN, Jose I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GUTTERSON, Neal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPETTI, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CANALES, Roger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RATCLIFFE, Oliver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KUMIMOTO, Roderick W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/10714887 o. US20060015972A1
                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biotechnology,
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                                                                                                                                                                                                                                                                                                                                    Score 59; DB Pred. No. 70; 4; Mismatches
                                                                                                                                                                                                                                                                                                                                           4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Orthologous to G2999
                                                                                                                                                                                                                                                                                                                                                                                   DB 5;
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APPLICANT: INCYTE GENOMICS, INC.; TANG, Y. Tom
APPLICANT: YUE, Henry; AZINZAI, Yalda
APPLICANT: HE, Ann; BATRA, Sajeev
APPLICANT: LO, Terence P.; NGUYEN, Danniel B.
APPLICANT: BURRILL, John D.; MARCUS, Gregory A.
APPLICANT: SURGLER, Kurt A.; GANDHI, Ameena R.
APPLICANT: ZINGLER, Kurt A.; GANDHI, Ameena R.
APPLICANT: BURFORD, Neil; YAO, Monique G.
APPLICANT: BURFORD, Neil; YAO, Monique G.
APPLICANT: CHAWLA, Narinder K.; ELLIOT, Vicki S.
APPLICANT: ARVIZU, Chandra S.; KHAN, Farrah A.
APPLICANT: BAUGHN, Mariah R.; HAFALIA, April, J.A.
APPLICANT: POLICKY, Jennifer L.; AU-YOUNG, Janice K.
APPLICANT: LU, Yan; BOROWSKY, Mark L.
APPLICANT: LU, Yan; BOROWSKY, Mark L.
APPLICANT: YANG, Junming; GURURALAN, Rajagopal
APPLICANT: YANG, Junming; GURURALAN, Rajagopal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-312-352-13
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                   CURRENT APPLICATION NUMBER: US/10/312,352
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: PCT/US01/21067
PRIOR FILING DATE: 2001-06-29
PRIOR APPLICATION NUMBER: US 60/215,454
PRIOR APPLICATION NUMBER: US 60/219,462
PRIOR APPLICATION NUMBER: US 60/219,462
PRIOR APPLICATION NUMBER: US 60/219,462
PRIOR FILING DATE: 2000-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: PCT/US01/18569
PRIOR FILING DATE: 2001-06-07
PRIOR PILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 4360
SOFTWARE: Patentin Ver: 3:1
SEQ ID NO 2829
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Publication No.
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                                                                                                                                                                                                                                       APPLICANT: WARREN, Bridget A.; GIETZEN, Kimberly J.
APPLICANT: XU, Yuming; KALLICK, Deborah A.
APPLICANT: LEE, Engles LEE, Langelo W.; HANGAVELD, Kavitha
APPLICANT: DELEGEANE, Angelo M.; LEE, Sally
TITLE OF INVENTION: EXTRACELLULAR MATRIX AND CELL ADHESION MOLECULES
FILE REFERENCE: PF-0794 USN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
NAME/KEY: MISC_FEATURE
LOCATION: (18)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: MISC_FEATURE LOCATION: (22)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Xaa equals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: MISC_FEATURE LOCATION: (9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Xaa equals any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: MISC_FEATURE LOCATION: (7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 604
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APPLICATION NUMBER: US 60/240,111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           529 VGGMPFSVYGNAMIPPVAPIP---DGA 552
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No. US20040053824A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 58.5; DB 4;
Pred. No. 1.5e+02;
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RESULT 11 US-10-032-585-7691

Sequence 7691, Application US/10032585
Publication No. US20030180953A1
GENERAL INFORMATION:
APPLICANT: Terry, Roemer D.
APPLICANT: Bo, Jiang

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PRIOR APPLICATION NUMBER: US 60/240,106
PRIOR FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: US 60/244,021
PRIOR PILING DATE: 2000-10-27
PRIOR PILING DATE: 2000-10-27
PRIOR REPLICATION NUMBER: US 60/248,887
PRIOR APPLICATION NUMBER: US 60/249,570
PRIOR APPLICATION NUMBER: US 60/249,570
PRIOR PILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PERL PROGram
SEQ ID NO 13
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US-10-745-237-260
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                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1 SEQ ID NO 260
                                                                           Matches
                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 260, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                             Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cyclacel Limited
APPLICANT: Glover, David
APPLICANT: Bell, Graham
APPLICANT: Frenz, Lisa
APPLICANT: Midgley, Carol
                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/745,237
CURRENT FILING DATE: 2003-12-23
PRIOR APPLICATION NUMBER: US 60/439,123
PRIOR FILING DATE: 2003-01-10
PRIOR APPLICATION NUMBER: US 60/468,402
                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Midgley, Carol
TITLE OF INVENTION: Cell Cycle Progression Proteins
FILE REFERENCE: P015819WO CYK
                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-10-12
                                                                                                                                                                                          TYPE: PRT ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20040053824A1 5773251CD1
                                                                                                                                                                        OTHER INFORMATION: 075179; BAA31672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 987
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2411 VGGMPFSVYGNAMIPPVAPIP---DGA 2434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               912 VGGMPFSVYGNAMIPPVAPIP---DGA 935
                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                  2 IGNLGNNVNGNHLIPPAPPLPSQTDGA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 IGNLGNNVNGNHLIPPAPPLPSQTDGA 28
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                                                                             Conservative
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                                                                                           35.5%;
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                                                                       5; Mismatches
                                                                                             Score 58.5; DB 5
Pred. No. 6.8e+02
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Pred. No. 2.6e+02
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                                                                                                               DB 5;
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                                                                                                               Length 2486;
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                                                                             Gaps
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NUMBER OF SEQ ID NOS: 50
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 2
LENGTH: 1026
TYPE: PRT
ORGANISM: C. elegans
US-10-415-656-2
                                                                                                                                                                                                                                                                                                                                                                               RESULT 13
US-09-835-232-2
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TITLE OF INVENTION: Gene Disruption Methodologies for Drug Target Discovery
FILE REFERENCE: 10182-005-999
; CURRENT APPLICATION NUMBER: US/10/032,585
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 8000
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7691
; SEQ ID NO 7691
; TYPE: PRT
; ORGANISM: Candida albicans
US-10-032-585-7691
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                                                      NUMBER OF SEQ ID NOS: 22
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/10415656
Publication No. US20050101773A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Leder, Philip
APPLICANT: Leader, Benja
                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/09835232 Patent No. US20020098489A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Best Local Similarity
                                                                                                                  CURRENT APPLICATION NUMBER: US/09/835,232
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: US 60/196,811
PRIOR FILING DATE: 2000-04-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cenix BioScience GmbH
TITLE OF INVENTION: Genes required for viability and/or reproduction
TITLE OF INVENTION: use in the development of anti-nematode agents
                                                                                                                                                                                                        APPLICANT: Leader, Benjamin
TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 00383/052002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/246,721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/415,656
CURRENT FILING DATE: 2003-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: CE61823US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Charles,
ORGANISM: Mus musculus
                                       ENGTH: 1567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17 NRHNSIGGNWHLPPPPPPPTQ 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 GNLGNNVNGNHLIPPAPPLPSQ 24
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47.6%;
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54.5%;
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Pred. No. 2.4e+02,
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 58; DB 5;
Pred. No. 3.1e+02;
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APPLICANT: Leder, Philip
APPLICANT: Leder, Benjamin
APPLICANT: Leder, Benjamin
TITLE OF INVENTION: FORMIN-2 NUCLEIC ACIDS AND POLYPEPTIDES
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: 00383/052002
CURRENT APPLICATION NUMBER: US/10/308,485
CURRENT FILING DATE: 2002-12-03
PRIOR APPLICATION NUMBER: US/09/835,232
PRIOR APPLICATION NUMBER: US/09/835,232
PRIOR FILING DATE: 2001-04-12
PRIOR FILING DATE: 2001-04-13
NUMBER OF SEQ ID NOS: 22
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                                                         ; OTHER INFORMATION: Clone ID: PAT_MRT4530_16297C.1.pep
US-10-437-963-112409
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                                                                                                                                                                 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NOS: 204966 SEQ ID NO 112409
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 112409, Application US/10437963 Publication No. US20040123343A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1567
TYPE: PRT
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                          ORGANISM: Oryza sativa FEATURE:
                                                                                                                                 TYPE: PRT
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                                                                                                                                                 LENGTH: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           831 SFGNNCN----VPPAPPLP 845
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Wei
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                                                                                                                                                                                                                                                                                                   Li, Ping
                                                                                                                                                                                                                                                                                                                   Barbazuk, Brad
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 34.8%;
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Pred. No.
 Score 57.5; DB 4; Pred. No. 21;
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Pred. No. 4.8e+02;
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                 Length 69;
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RESULT 17
US-09-879-957-67
; Sequence 67, Application US/09879957
; Patent No. US20020034755A1
; GENERAL INFORMATION:
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US-11-097-143-1062
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; ORGANISM: DROSOPHILA
US-11-097-143-1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILLING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILLING DATE: 1999-10-19
PRIOR PELICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
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Tocal Similarity
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Publication No. US20050208558A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1062
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CL000728
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                        McCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/173,383
                                                                                                                                                                                                                                                                      APPLICANT: SPARKS, Andrew B.
HOFFMAN, No. US20020034755A1h
                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             84 GKNGFQASGDHLPQAPPAPPQPVPTAG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GNLGNNVNGNHL--IPPAPPLPSQTDG 27
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                                        STREET: 1155 Avenue of the Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGGL----GGHQAPPAPPLPEGIGG 21
                       STATE: New York
    COUNTRY: USA
                                                                                   ADDRESSEE: Pennie & Edmonds LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                      KAY, Brian K.
                                                                                                                                                                                                                             FOWLKES, Dana M.
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                                                                                                                                                USING SAME
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Pred. No. 88;
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OTHER INFORMATION: Biotinylated N-terminal;
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-879-957-67
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US-10-807-856-67
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 67: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEPAX: (212) 790-9090
TELEPAX: (212) 780-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION UNMBER: US/09/879,957

FILING DATE: 13-Unn-2001

CLASSIFICATION: <Unknown>
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/807,856
FILING DATE: 23-Mar-2004
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                KAY, Brian K.
FOWLKES, Dana M.
MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: SPARKS, Andrew B.
HOFFMAN, Noah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide
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                                                                                                                                                                                                                               CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                      COUNTRY: USA
ZIP: 10036-2711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 10036-2711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US20040157216A1
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APPLICANT: Allen, George P
TITLE OF INVENTION: Viral Marker
FILE REFERENCE: 620-262
CURRENT APPLICATION NUMBER: US/10/626,832
CURRENT FILING DATE: 2003-07-25
PRIOR APPLICATION NUMBER: US 60/398,576
PRIOR FILING DATE: 2002-07-26
NUMBER OF SEQ ID NOS: 259
SOFTWARE: Patentin version 3.1
SEQ ID NO 157
LENGTH: 42
TYPE: DRT
                              RESULT 20
US-10-424-599-249972
; Sequence 249972, Application US/10424599
; Publication No. US20040031072A1
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                                                                                                                                                                                                                                                                                                ; ORGANISM: Equine herpesvirus 1 US-10-626-832-157
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                                                                                                                                                                                                          Query Match
Best Local Similarity 66.7
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APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 66141 PENNIE INFORMATION FOR SEQ ID NO: 67: SEQUENCE CHARACTERISTICS: LENGTH: 22 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: Other
OTHER INFORMATION: Biotinylated N-terminal
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                        15 IPPAPPLPSQTDGAA 29
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                                                                                                                                                        3 LPPAPPLPQSTSKAA 17
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TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/630,915 FILING DATE: 03-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birch-Machin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/10626832
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 Mismatches

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Pred. No. 8.
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Pred. No.
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Publication No. US20040259145A1
GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Wood, Michael A.
APPLICANT: MoGrath, Annette
APPLICANT: Glenn, Matthew
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US-10-856-499-794
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                                                                                                                                                                                                      Sequence 189120, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
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SEQ ID NO 249972
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Best Local Similarity
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
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CURRENT FILING DATE: 2003-04-28
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                                                                                                             Zhou, Yihua
Cao, Yongwei
Wu, Wei
Boukharov, Andrey A.
Barbazuk, Brad
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/10856499
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Pred. No. 6
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                                                                                    Associated With
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION UNBER: US/10/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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                                                              US-10-369-493-21572
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-369-493-21572
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: GOCAL, GREG
TITLE OF INVENTION: NON-TRANSGENIC HERBICIDE RESISTANT PLANTS
FILE REFERENCE: CAL138
CURRENT APPLICATION NUMBER: US/10/214,766
CURRENT FILING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: US/0/311,734
PRIOR APPLICATION NUMBER: US/0/311,734
PRIOR FILING DATE: 2001-08-09
NUMBER OF SEQ ID NOS: 53
COUNTY NUMBER OF SEQ ID NOS: 53
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LENGTH: 187
                                                                         SEQ ID NO 21572
LENGTH: 410
TYPE: PRT
ORGANISM: Pyrococcus abyssi
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 21572, Application US/10369493 Publication No. US20030233675A1
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Query Match
Best Local Similarity
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Best Local Similarity
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Best Local Similarity 58.8%;
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   33.9%;
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Pred. No.
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Pred. No.
     Score
Pred.
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     . No.
     DB 4;
2e+02;
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2e+02;
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SOPTWARE: PatentIn version 3.1
SEQ ID NO 27
LENGTH: 3402
TYPE: PRT
ORGANISM: Equine herpesvirus 1
US-10-626-832-27
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; Sequence 27, Application US/10626832
; Publication No. US20050003342A1
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                                                                                                                                               ; OTHER INFORMATION: Clone ID: PAT_MRT3847_49002C.1.pep US-10-424-599-229211
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 229211
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                                                                         Matches
                                                                                           Query Match
Best Local :
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APPLICANT: Nugent, Josephine
APPLICANT: Birch-Machin, Ian
APPLICANT: Allen, George P
TITLE OF INVENTION: Viral Marker
                                                                                                                                                                                                                                                                                                                                    APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/398,576
PRIOR FILING DATE: 2002-07-26
NUMBER OF SEQ ID NOS: 259
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CURRENT APPLICATION NUMBER: US/10/626,832
CURRENT FILING DATE: 2003-07-25
                                                                                                                                                                              TYPE: PRT
ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                          LENGTH: 167
                                                                       Local Similarity es 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2549 LPPAPPLPQSTSKAA 2563
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 61
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                           PIGNLGNNVNGNHLI----PPAPPLPSQ 24
PTPNTTTNNNNNLIQTNTNPPSPPPPPQ 89
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                                                                         Conservative
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                                                                                           33.6%;
44.8%;
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                                                                                         Score 55.5;
Pred. No. 90
                                                                         Mismatches
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                                                                                               90;
                                                                                                            DB 4;
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RESULT 27 US-10-739-930-9050

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US-11-150-845-47
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                 Sequence 12, Application US/10606060A Publication No. US20040058369A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Pierce, Daniel
APPLICANT: Finer, Jeffrey
TITLE OF INVENTION: HIGH THROUPUT ACTIN POLYMERIZATION ASSAY
FILE REFERENCE: 020552-007720US
CURRENT APPLICATION NUMBER: US/11/150,845
CURRENT FILING DATE: 2005-06-10
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TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILLING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
APPLICANT: Syngenta
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PRIOR FILING DATE: 2004-06-10
NUMBER OF SEQ ID NOS: 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 627
TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                 LOCATION: (1). (627)
OTHER INFORMATION: FOR1 FH1-FH2 domain
                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(627)
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ORGANISM: Glycine max
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                                                                                                                                                                                                                                            Similarity
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Jia, Zhiheng
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55.0%;
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Pred. No. 3.6e
4; Mismatches
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Pred. No. 1.7e+02;
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RESULT 31
US-10-739-930-10284
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Sequence 10284, Application US/10739930

Publication No. US20040216190A1

GENERAL INFORMATION:
APPLICANT: Kovalic, David K.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53377)B

CURRENT APPLICATION NUMBER: US/10/739,930

CURRENT FILING DATE: 2003-12-18

NUMBER OF SEQ ID NOS: 11088

SEQ ID NO 10284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
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SEQ ID 00 291796
LENCTH: 223
TYPE: PRT
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Best Local Similarity
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APPLICANT:
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CURRENT FILING DATE: 2003-04-28
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PRIOR FILING DATE: 1996-05-24
PRIOR APPLICATION NUMBER: US 09/564,418
PRIOR FILING DATE: 2000-05-03
NUMBER OF SEQ ID NOS: 59
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APPLICANT: Greenland, Andrew James
TITLE OF INVENTION: A GENE SWITCH
FILE REFERENCE: 1392/4/3/2
CURRENT APPLICATION NUMBER: US/10/606,060A
CURRENT FILING DATE: 2003-06-25
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TYPE: PRT
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Local Similarity 52.0%;
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Pred. No. 3.9e
2; Mismatches
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Pred. No. 1.4e
2; Mismatches
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5;
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LENGTH:

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Query Match
Best Local Similarity
Thes 12; Conserve
                                                                               ; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-10-282-122A-64954
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US-10-282-122A-64954
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US-10-739-930-10284
                                                                                                                                                              Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO 64954
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Publication No. US20040029129A1
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PRIOR FILING DATE: 2000-03-21
PRIOR ADDITOR TO TAKE TO THE PRIOR ADDITOR TO TAKE TO THE PRIOR ADDITOR TO THE PRIOR ADDITOR TO THE PRIOR ADDITOR TO THE PRIOR ADDITOR TO THE PRIOR ADDIT
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CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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PRIOR FILING DATE: 2000-05-23
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NAME/KEY: unsure
LOCATION: (1)..(319)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                ENGTH: 598
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Local Similarity 56.2%;
hes 9; Conservation
                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/267,636 FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 2000-10-23
APPLICATION NUMBER: 60/253,625
                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/242,578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/230,335
                                                                                                                                                                                                                                                                                                                 FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/257,931
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/230,347 FILING DATE: 2000-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 2000-09-06
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: Zamudio, Carlos
: Malone, Cheryl
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                   Conservative
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                                33.3%;
               Score 55; DB Pred. No. 4e+0:
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Pred. No. 2.1e+02;
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                                  DB 4;
4e+02;
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                                                    Length 598;
                   Indels
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                 Gaps
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US-10-425-115-242739
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US-10-437-963-140066
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US-10-437-963-140066
                                                                        Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53221)B CURRENT APPLICATION NUMBER: US/10/437,963 CURRENT FILING DATE: 2003-05-14 NUMBER OF SEQ ID NO 140066 SEQ ID NO 140066 LENGTH: 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 242739, Application US/10425115 Publication No. US20040214272A1 GENERAL INFORMATION:
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APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 242739
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                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
TITLE OF INVENTION: Plants
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
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ORGANISM: Oryza sativa
                                                                                                                                                             OTHER INFORMATION: Clone ID: MRT4577_152961C.1.per
                                                                                                                                                                                              TYPE: PRT
ORGANISM: Zea mays
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                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                           ENGTH: 198
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 44
                                   16 PPAPP-LPSQTDGAAR 30
                                                                        l Similarity
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Wu, Wei
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Cao, Yongwei
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                                                                      33.0%; Score 54.5; DB 4; Length 198; llarity 75.0%; Pred. No. 1.4e+02; Conservative 1; Mismatches 2; Indels
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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_77732C.1.pep
US-10-437-963-180357
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                                                                           ; NUMBER OF SEQ ID NOS: 204
SEQ ID NO 180357
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Oryza sativa
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CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR PRIOR APPLICATION NUMBER: 60/160,191
PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-10-28
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-11-28
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-28
PRIOR FILING DATE: 1999-12-28
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Best Local Similarity
Matches 11; Conserv
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 31545
LENGTH: 283
                                                                                                                                                          APPLICANT: Li, Ping
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)8
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
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APPLICANT:
APPLICANT:
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Publication No. US20050208558A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: La Rosa, Thomas J. APPLICANT: Kovalic, David K. APPLICANT: Zhou, Yihua
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APPLICANT: et al.
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CL000728
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PRIOR FILING DATE: 2000-03-23
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PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
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Cao, Yongwei
Wu, Wei
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Barbazuk, Brad
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45.8%; Pred. No. 2.1e+02;
ative 3; Mismatches 3;
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APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei

ITITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

PLIE REFERENCE: 38-21 (53535)B

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT FILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

ENGTH: 202

TYPE: No.
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                                                                                                                                              ; ORGANISM: Homo sapiens
US-10-108-260A-4737
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US-10-767-701-59871
                                                                                                                                                                                                APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. US20040005560A1el full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4737
LENGTH: 279
                                                                                                                                                                                                                                                                                                                                                                    Sequence 4737, Application US/10108260A Publication No. US20040005560A1 GENERAL INFORMATION:
                                                                     Query Match 32.7%; Score 54; I Best Local Similarity 47.6%; Pred. No. 2 Matches 10; Conservative 3; Mismatche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 PPSPQLPTQVDGA 196
 95
                                    10 NGNHLIPPAPPLPSQTDGAAR 30
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SGKLISPPVPPRPTQTASPAR 115
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69.2%; Pred. No. 1.7e+02;
ative 2; Mismatches 2
                                                                         Mismatches
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RESULT 39 US-10-425-114-72305

Sequence 72305, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:

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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(3313)B
CURRENT FILLING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 72305
LENGTH: 319
TYPE: PRI
ORGANISM: Zea mays
FEATURE:
ORGANISM: Zea mays
FEATURE:
OTHER INFORMATION: Clone ID: UC-ZMFLB73119E02_FLI.pep
US-10-425-114-72305
Search completed: August 1, 2006, 22:02:10 Job time : 183 secs
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US-10-424-599-167611
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US-10-424-599-167611
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APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT EILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 167611
LENGTH: 359
TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                  Query Match
Best Local Similarity
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Publication No. US20040031072A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(359)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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                                                                                       88 HRTNPNPLLAPLPPIPSPAVGSA 110
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                                                                                                                            7 NNVNGNHLIPPAPPLPSQTDGAA 29
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                                                                                                                                                                          32.7%;
ilarity 43.5%;
Conservative
                                                                                                                                                                        Score 54; DB 4; Length 359; Pred. No. 3.1e+02; 4; Mismatches 9; Indels
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Title:
Perfect score:
Sequence:
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No
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Maximum DB
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; TYPE: PRT; ORGANISM: Oryza sativa US-10-449-902-45343
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; TYPE: PRT
; ORGANISM: Oryza sativa
US-10-449-902-38007
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Publication No. US20060123505A1
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PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
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CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
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APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.
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PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
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US-10-449-902-41370
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US-10-449-902-52811
Sequence 3920, Application US/11174307B
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SEQ ID NO 41370
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Publication No. US20060123505A1
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SEQ ID NO 52811
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APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Ephysical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT APPLICATION NUMBER: US/202-203269
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-383870
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CURRENT FILLING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
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APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
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                                                                                                                                                                                                                            Score 56; DB 6; Pred. No. 6.1;
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Pred. No. 10;
                                                                                                                  80
                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                 Length 118;
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                                                                                                                                                                                                        Indels
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; OTHER INFORMATION: GI Number: 50940371; NR Description: putative pherophorin-dz1; OTHER INFORMATION: protein [Oryza sativa (japonica cultivar-group)]; OTHER INFORMATION: >gi|42408241|dbj|BAD09398.1| putative pherophorin-dz1 protein US-11-174-3078-3920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 5544
SEQ ID NO 3920
LENGTH: 159
                                                                              Matches
                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Publication No. US20060143729A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/583,781
PRIOR FILING DATE: 2004-06-30
PRIOR APPLICATION NUMBER: 60/583,651
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CURRENT FILING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: 60/583,671
PRIOR FILING DATE: 2004-06-30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NUCLEOTIDE SEQUENCES AND POLYPEPTIDES TITLE OF INVENTION: USEFUL FOR MODIFYING PLANT CHARACTERI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheslav
                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: GI Number: 50938941; NR Description: putative diaphanous OTHER INFORMATION: homologue [Oryza sativa (japonica cultivar-group)]
                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: GI Number: 20420; NR Description: extensin [Prunus dulcis]
THER INFORMATION: >gi|99861|pir||S20790 extensin - almond >gi|445616|prf||1909363A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: GI Number: 6523547; NR Description: hydroxyproline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: >gi|27817931|dbj|BAC55695.1] putative diaphanous homologue [Oryz:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: PFam Name: GATase_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
OTHER INFORMATION: PFam Name: LMBR1; PFam Description: LMBR1-like membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
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OTHER INFORMATION: PFam Name: FH2; PFam Description: Formin Homology 2 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
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10 NGNHLIPPAPPLPSQTDGAAR 30
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                                                                                              33.9%;
                                                                         0,
                                                                                                 Score 56;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Extensin_2; PFam Description: Extensin-like region
                                                                            Mismatches
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                                                                                                                           DB 7;
                                                                         9;
                                                                                                                           Length 159;
                                                                            Indels
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; ORGANISM: Mycosphaerella pini
US-11-063-439-228
                                                      SOFTWARE: Pac
SOFTWARE: Pac
SEQ ID NO 228
FORGTH: 3491
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                                                                                                                                                     PRIOR APPLICATION NUMBER: 10/923,615
PRIOR FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: 60/516,134
PRIOR FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: 10/808,618
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 10/867,517
PRIOR FILING DATE: 2004-06-14
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LENGTH: 3488
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: TUSZYNSKI, JACK A.
APPLICANT: GREENWALD, HOWARD
APPLICANT: CURRY, STEPHEN H.
APPLICANT: GOSS, KENDRICK
                                                                                                                                    PRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 418
                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/11/063,439
CURRENT FILING DATE: 2005-02-23
PRIOR APPLICATION NUMBER: 10/878,905
PRIOR FILING DATE: 2004-06-28
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PRIOR APPLICATION NUMBER: 10/867,517
PRIOR FILING DATE: 2004-06-14
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PRIOR APPLICATION NUMBER: 60/516,134
PRIOR FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: 10/808,618
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CURRENT APPLICATION NUMBER: US/11/063,439
CURRENT FILING DATE: 2005-02-23
PRIOR APPLICATION NUMBER: 10/878,905
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APPLICANT: GREENWALD, HOWARD
APPLICANT: CURRY, STEPHEN H.
APPLICANT: GOSS, KENDRICK
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PRIOR APPLICATION NUMBER: 10/923,615
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Similarity 44.0%; Pred. No.
                                                                                                               PatentIn version 3.3
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D. US20060147371A1
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5. US20060147371A1
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Query Match
Best Local Similarity
"``+ hes 9; Conserva
                                                                                           ; ORGANISM: Triticum aestivum US-10-953-349-25635
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TYPE: PRT
; ORGANISM: Phaeosphaeria nodorum
US-11-063-439-236
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PRIOR FILLING DATE: 2004-08-20
PRIOR PRIOR PRIOR NUMBER: 60/516,134
PRIOR FILLING DATE: 2003-10-31
PRIOR FILLING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: 10/808,618
PRIOR FILLING DATE: 2004-03-24
PRIOR FILLING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 418
NUMBER OF SEQ ID NOS: 418
                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 25635
LENGTH: 109
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Best Local Similarity
Matches 11; Conserv
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Best Local Similarity 44.0%;
Matches 11; Conservative
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CURRENT APPLICATION NUMBER: US/11/063,439
CURRENT FILING DATE: 2005-02-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 10/878,905 PRIOR FILING DATE: 2004-06-28
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                                                                                                                                 TYPE: PRT
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GOSS, KENDRICK
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ilarity 44.0%;
Conservative
                   Conservative
                                   33.3%;
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; Pred. No. 2e+0;
3; Mismatches
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Pred. No. 2.1e+02
                                   Score 55; DB
Pred. No. 7.4;
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                   Mismatches
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2e+02;
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US-11-063-439-119
; Sequence 119, Application US/11063439
; Publication No. US20060147371A1
; GENERAL INFORMATION:
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US-10-953-349-29057
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 29058
LENGTH: 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY FILE REFERENCE: 2750-1579PUS2 CURRENT APPLICATION NUMBER: US/10/953,349 CURRENT FILING DATE: 2004-09-30 NUMBER OF SEQ ID NOS: 40252 SOFTWARE: PatentIn version 3.3 SEQ ID NO 29057 LENGTH: 346
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APPLICANT: ALEXANDROV, Nickolai et al.

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

FILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 29057, Application US/10953349 Publication No. US20060107345A1
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                               APPLICANT: TUSZYNSKI, JACK A.
APPLICANT: GREENWALD, HOWARD J.
APPLICANT: CURRY, STEPHEN H.
APPLICANT: GOSS, KENDRICK
TITLE OF INVENTION: WATER-SOLUBLE COMPOUND
                   FILE REFERENCE:
 CURRENT APPLICATION NUMBER: US/11/063,439
                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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nes 9; Conserv
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                     1034312-000027
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Pred. No. 22;
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Pred. No.
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US-11-063-439-290
, Sequence 290, Application US/11063439
; Publication No. US20060147371A1
; GENERAL INFORMATION:
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                                                                                    RESULT 14
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PRIOR FILING DATE: 2004-06-28
PRIOR APPLICATION NUMBER: 10/923,615
PRIOR FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: 60/516,134
PRIOR FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: 10/808,618
PRIOR FILING DATE: 2004-03-24
PRIOR FILING DATE: 2004-03-24
PRIOR FILING DATE: 2004-03-24
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US-11-063-439-119
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PRIOR FILING DATE: 2004-06-28
PRIOR PELICATION NUMBER: 10/923,615
PRIOR FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: 60/516,134
PRIOR FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: 10/808,618
PRIOR FILING DATE: 2004-03-24
PRIOR FILING DATE: 2004-03-24
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Best Local Similarity
Matches 11; Conserv
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SEQ ID NO 284
LENGTH: 3617
TYPE: PRT
TYPE: PRT
ORGANISM: Plasmodium falciparum
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Best Local
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LENGTH: 3504
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CURRENT APPLICATION NUMBER: US/11/063,439
CURRENT FILING DATE: 2005-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: TUSZYNSKI, JACK A.
APPLICANT: GREENWALD, HOWARD J.
APPLICANT: CURRY, STEPHEN H.
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NUMBER OF SEQ ID NOS: 418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 10/867,517
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PRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 418
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GOSS, KENDRICK
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 Mismatches

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Pred. No. 2.7e+02;
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RESULT 16
US-10-953-349-24737
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US-10-953-349-24738
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APPLICANT: GORRY, STEPHEN H.
APPLICANT: GOSS, KENDRICK
TITLE OF INVENTION: WATER-SOLUBLE COMPOUND
FILE REFERENCE: 1034312-000027
CURRENT APPLICATION NUMBER: US/11/063,439
CURRENT FILING DATE: 2005-02-23
PRIOR APPLICATION NUMBER: 10/879,905
PRIOR FILING DATE: 2004-06-28
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PRIOR FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: 60/516,134
PRIOR FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: 10/808,618
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 10/867,517
PRIOR APPLICATION NUMBER: 10/867,517
PRIOR FILING DATE: 2004-06-14
                  Sequence 24737, Application US/10953349
Publication No. US20060107345A1
GENERRAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 24738
LENGTH: 277
TYPE: PRT
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LENGTH: 3700
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Best Local Similarity
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Best Local
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TITLE OF INVENTION: SEQUENCE-DETERMINED DI
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579US2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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SOFTWARE: PatentIn version
CURRENT APPLICATION NUMBER: US/10/953,349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Saccharomyces cerevisiae
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                                                                                                                                                                                                                                                           HRTNPNPLLAPLPPIPSPAVGSA 109
                                                                                                                                                                                                                                                                                                                                              32.7%; Score 54; DB ilarity 43.5%; Pred. No. 26; Conservative 4; Mismatches
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                       Length 277;
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NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 24737
LENGTH: 278
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-24737
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APPLICANT: HELIX RESEARCH INSTITUTE
APPLICANT: HELIX RESEARCH INSTITUTE
ITITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4737
LENGTH: 279
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US-10-953-349-24736
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US-11-293-697-4737
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                                                                                                                        US-10-953-349-24736
                                                                                                                                                                                                                                                                                                                         Sequence 24736, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                                                                                                    SOFTWARE: PatentIn version 3.3 SEQ ID NO 24736
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Best Local Similarity
                                                             Matches
                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                              APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
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                                                                                                                                     LENGTH: 296
TYPE: PRT
ORGANISM: Glycine max
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                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         95
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HRTNPNPLLAPLPPIPSPAVGSA 128
                           NNVNGNHLIPPAPPLPSQTDGAA 29
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                                                            Conservative
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43.5%;
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43.5%;
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                                                                       Score 54;
Pred. No.
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Pred. No.
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Pred. No.
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26;
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27;
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; NAME/KEY: peptide
; LCCATION: (1) .. (139)
; OTHER INFORMATION: Cerres Seq.
US-11-056-355B-61177
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                                                                                                                                    RESULT 21
US-10-449-902-43015
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US-10-953-349-26514
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 42052
SOFTWARE: PatentIn version 3.3
SEQ ID NO 26514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding TITLE OF INVENTION: Polypeptides Encoded Thereby FILE REFERENCE: 2750-1590PUS2 CURRENT APPLICATION NUMBER: US/11/056,355B CURRENT FILING DATE: 2005-02-14 PRIOR APPLICATION NUMBER: 60/544,190 PRIOR APPLICATION NUMBER: 60/544,190 PRIOR PILING DATE: 2004-02-13 NUMBER OF SEQ ID NOS: 119966 SEQ ID NO 61177 LENGTH: 139
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Publication No. US20066107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
                                                                       Sequence 43015, Application US/10449902 Publication No. US20060123505A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institute of Physical and Chemical Research.
APPLICANT: Foundation for Advancement of International Science.
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TYPE: PRT
ORGANISM: Triticum
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ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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les 9; Conserv
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81.8%;
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US-10-449-902-43015
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Best Local Similarity 62.5
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TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypepides Encoded Thereby
FILE REFERENCE: 2750-1530PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 97135
                                                                                                                                   Sequence 97134, Application US/11056355B
Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
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PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 43015
LENGTH: 228
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Best Local Similarity
                           TITLE OF INVENTION: Sequence Determined DNA Fragments and TITLE OF INVENTION: Polypeptides Encoded Thereby FILE REPERENCE: 2750-1590PUS2 CURRENT APPLICATION NUMBER: US/11/056,355B CURRENT FILING DATE: 2005-02-14
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CURRENT FILING DATE: 2003-05-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KRY: peptide
LOCATION: (1)..(427)
OTHER INFORMATION: Ceres Seq. ID no. 12736152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 427
TYPE: prt
ORGANISM: Arabidopsis thaliana
APPLICATION NUMBER: 60/544,190 FILING DATE: 2004-02-13
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Pred. No.
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RESULT 25
US-10-374-780A-2556
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US-10-449-902-48393
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APPLICANT: Sherman, Bradley K
APPLICANT: Riechmann, Jose Luis
APPLICANT: Jiang, Cai-Zhong
APPLICANT: Heard, Jacqueline E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 48393
LENGTH: 517
TYPE: PRT
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SEQ ID NO 97134
LENGTH: 452
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Best Local Similarity 44.0%;
Matches 11; Conservative :
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Publication No. US20060123505A1
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Best Local Similarity
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APPLICANT:
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APPLICANT: Bio-oriented Technology Research Advancement Ins
APPLICANT: The Institute of Physical and Chemical Research
APPLICANT: Foundation for Advancement of International Scientifle OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT FILING DATE: 2003-05-29
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ORGANISM: Arabidopsis thaliana
FEATURE:
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Pineda, Omaira
                 Pilgrim, Marsha L
Dubell III, Arnold T
                                                   Keddie, James
Broun, Pierre E
                                                                                       Reuber, T. Lynne
                                                                                                             Adam, Luc J
                                                                                                                                 Ratcliffe,
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                                                                                                                                                                       Haake, Volker
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APPLICANT: Yu, Guo-Liang
TITLE OF INVENTION: POLYMUCLEOTIDES AND POLYPEPTIDES IN PLANTS
FILE REFERENCE: MBI-0047 CIP

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                                                                                                                       ; FEATURE:
; NAME/KEY: peptide;
; LOCATION: (1)..(612)
; OTHER INFORMATION: Ceres Seq. ID
US-11-056-355B-97133
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US-11-056-355B-97133
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PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 97133
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 97133, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
                                                        Matches
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                                                                     Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding TITLE OF INVENTION: Polypeptides Encoded Thereby FILE REFERENCE: 2750-1590PUS2
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PRIOR
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PRIOR FILING DATE: 2001-04-18
PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
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                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Brover, Vyacheslav APPLICANT: Alexandrov, Nickolai
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PRIOR FILING DATE: 2002-08-09
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                                                                                                                                                                                                     TYPE: prt
ORGANISM: Arabidopsis thaliana
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APPLICATION NUMBER: 60/338,692
FILING DATE: 2001-12-11
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APPLICATION NUMBER: 10/
FILING DATE: 2002-08-09
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10 NGNHLIPPAPPLPSQT 25
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                                                                       Similarity
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                                                      Conservative
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Pred. No.
                                                                       Score 53;
Pred. No.
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                                                                                                                                           no.
                                                        Mismatches
                                                                                                                                              12736150
                                                                                       DB 7;
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                                                      Indels
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; NAME/KEY: peptide
; LOCATION: (1)..(1499)
; OTHER INFORMATION: Ceres Seq. ID no. 12646479
US-11-056-355B-78879
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US-11-056-355B-78879
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US-11-056-355B-85230
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TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Sequence Determined Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 85230
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                                                                                                                                                                                                                                                                                                                            SEQ ID NO 78879
LENGTH: 1499
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Best Local :
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                                                                                                                            Query Match
                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding TITLE OF INVENTION: Polypeptides Encoded Thereby FILE REFERENCE: 2750-1590US2 CURRENT APPLICATION NUMBER: US/11/056,355B CURRENT FILING DATE: 2005-02-14 PRIOR APPLICATION NUMBER: 60/544,190 PRIOR APPLICATION NUMBER: 60/544,190 PRIOR APPLICATION NUMBER: 60/544,190 PRIOR FILING DATE: 2004-02-13 NUMBER: 0F SEQ ID NOS: 119866
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LOCATION: (1)..(1481)
OTHER INFORMATION: Ce
                                                                                                                                                                                                                                                                                   TYPE: prt
ORGANISM: Arabidopsis thaliana
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ORGANISM: Arabidopsis thaliana
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472
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                                          3 GNLGNNVNGNHLIPPAPPLPSQ 24
GKSGRWMKGYHLKVPPPPLPPQ 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alexandrov, Nickolai
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                                                                                   Conservative
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                                                                                                       32.1%;
50.0%;
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50.0%;
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                                                                                                          Score 53; DB 7;
Pred. No. 1.9e+02
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Pred. No. 1.9e+02;
                                                                                     Mismatches
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                                                                                                                              Length 1499;
                                                                                          Indels
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RESULT 29 US-11-056-355B-85229

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RESULT 31
US-11-056-355B-78878
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Sequence 78878, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION: APPLICANT: Brover, Vyacheslav APPLICANT: Alexandrov, Nickolai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 85228
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LENGTH: 1510
                                                                                                                                                                                                                                                                                                         Query Match
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TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
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FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
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                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: peptide
LOCATION: (1)..(1520)
OTHER INFORMATION: Ceres Seq. ID no. 12679558
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ORGANISM: Arabidopsis thaliana
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OTHER INFORMATION: Ceres Seq. ID no. 12679559
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NAME/KEY: peptide
LOCATION: (1)..(1)
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ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                  Score 53;
Pred. No.
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                                                                                                                                                                                                                                                                                    2e+02;
                                                                                                                                                                                                                                                                                                    DB 7; Length 1520;
                                                                                                                                                                                                                                                               10;
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                                                                                                                                                                                                                                                               Indels
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PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 78877
LENGTH: 1538
TYPE: prt
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
NAME/KEY: peptide
NAME/KEY: peptide
OTHER INFORMATION: Ceres Seq. ID no. 12646477
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US-11-056-355B-96434
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; LOCATION: (1)..(1528)
; OTHER INFORMATION: Ceres Seq. ID no. 12646478
US-11-056-355B-78878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-11-056-355B-78877
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Sequence 96434, Application US/11056355B
Publication No. US20060150283A1
GENERAL INFORMATION:
APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION UNMERR: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 78877, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Fragments and
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
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ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                       511 GKSGRWMKGYHLKVPPPPLPPQ 532
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Pred. No. 2e+02;
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; TYBE: prt
; TYBE: prt
; TRATUISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(1568)
; OTHER INFORMATION: Ceres Seq. ID no. 12733266
US-11-056-355B-96434
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; NAME/KEY: peptide
; LOCATION: (1).. (1597)
; OTHER INFORMATION: Ceres Seq. ID no. 12733265
US-11-056-355B-96433
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US-11-056-355B-96433
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LENGTH: 1597
TYPE: prt
ORGANISM: Arabidopsis thaliana
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LENGTH: 1568
             PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 96432
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Best Local Similarity 50.0%;
Matches 11; Conservative
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                                                                                           APPLICANT: Brover, Vyacheslav
APPLICANT: Alexandrov, Nickolai
TITLE OF INVENTION: Sequence Determined DNA Pragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590FUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
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TITLE OF INVENTION: Sequence Determined DNA Fragments and Corresponding
TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590PUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
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PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
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LENGTH: 1607
                                                                                                                                                                                                                                                                                                                                                                                                          570 GKSGRWMKGYHLKVPPPPLPPQ 591
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Pred. No. 2.1e+02;
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APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53629)B
CURRENT APPLICATION NUMBER: US/11/330,403
CURRENT FILING DATE: 2006-01-12
UNMBER OF SEQ ID NOS: 19250
SEQ ID NO 11014
LENGTH: 1832
TYPE: PRT
ORGANISM: Podospora anserina
US-11-330-403-11014
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; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-31117
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US-10-953-349-31117
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US-11-330-403-11014
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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Publication No. US20060159563A1
GENERAL INFORMATION:
                                                                                    Query Match
Best Local Similarity
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Best Local (
                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
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LOCATION: (1)..(1607)
OTHER INFORMATION: Ceres Seq. ID no. 12733264
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ORGANISM: Arabidopsis thaliana
FEATURE:
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Local Similarity 45.5%;
les 10; Conservative
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17 GNGVYANHEIIPPPPLSLQ 35
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                                6 GNNVNGNHLIPPAPPLPSQ 24
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                                                                    Conservative
                                                                                    31.5%;
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50.0%;
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Pred. No. 2.4e+02
                                                                                    Score 52; DB
Pred. No. 14;
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Pred. No. 2.1e+02;
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                                                                      Mismatches
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RESULT 38 US-10-449-902-31399

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APPLICANT: National Institute of Agrobiological Sciences.
APPLICANT: Bio-oriented Technology Research Advancement Institution.
APPLICANT: The Institute of Physical and Chemical Research.
APPLICANT: Toundation for Advancement of International Science.
TITLE OF INVENTION: FULL-LENGTH PLANT cDNA AND USES THEREOF
FILE REFERENCE: MOA-A0205Y1-US
CURRENT APPLICATION NUMBER: US/10/449,902
CURRENT PILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR APPLICATION NUMBER: JP 2002-383870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: JP 2002-203269
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: JP 2002-383870
PRIOR FILING DATE: 2002-12-11
NUMBER OF SEQ ID NOS: 56791
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 54720
LENGTH: 788
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US-10-519-342-3
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Sequence 3, Application US/10519342
Publication No. US20060160729A1
GENERAL INFORMATION:
APPLICANT: Li, Dean
APPLICANT: Park, Kye Won
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Best Local S
Matches 9
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Publication No. US20060123505A1

GENERAL INFORMATION:

APPLICANT: National Institute of Agrobiological Sciences.

APPLICANT: Bio-oriented Technology Research Advancement Institution.

APPLICANT: The Institute of Physical and Chemical Research.

APPLICANT: Foundation for Advancement of International Science.

TITLE OF INVENTION: FULL-LENGTH PLANT CDNA AND USES THEREOF

FILE REFERENCE: MOA-0205Y1-US

CURRENT APPLICATION NUMBER: US/10/449,902

CURRENT FILING DATE: 2003-05-29

BERTOR ADDITORTION NUMBER: TO 2003-05-29

BERTOR ADDITORTION NUMBER: TO 2003-05-29

BERTOR ADDITORTION NUMBER: TO 2003-05-29
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SEQ ID NO 31399
LENGTH: 112
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ORGANISM: Oryza sativa
;-10-449-902-31399
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Publication No. US20060123505A1
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                                                                                                                                                                                                                                                                                                                       16 PPAPPLPSQTDGAA 29
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR MANIPULATING THE GUIDED TITLE OF INVENTION: NAVIGATION OF ENDOTHBLIAL TUBES DURING ANGIOGENESIS FILE REFERENCE: UUTH-PO1-010

CURRENT FILING DATE: 2004-12-21

PRIOR APPLICATION NUMBER: G0/392,142

PRIOR FILING DATE: 2002-06-27

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin version 3.1

SEQ ID NO 3

LENGTH: 1012

TYPE: PRT

COGGANISM: Mouse

US-10-519-342-3

Query Match
Best Local Similarity 44.4%; Pred. No. 1.7e+02;

Matches 12; Conservative 6; Mismatches 7; Indels 2; Gaps 2;

Matches 12; Conservative 6; Mismatches 7; Indels 2; Gaps 2;

Search Completed: August 1. 2006 22.02.45

Search Completed: August 1. 2006 22.02.45
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Search completed: August 1, 2006, 22:02:45
Job time : 31 secs

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Title:
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
       Score
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ALIGNMENTS

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gasawara, N.; Yasunaga, 1.; Numuru, 2...
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
Personne number: A99629; MUID:21156231; PMID:11258796
                A;Title: Prediction of the coding sequences of unidentified A;Reference number: Z14142; MUID:98403880; PMID:9734811 A;Accession: T00353
                                                                                                                            hypothetical protein KIAA0697 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-558 <HAY>
A;Residues: 1-558 <HAY>
A;Cross-references: UNIPROT:Q9R396; UNIPARC:UPI00000D00CA; GB:BA000007;
A:Experimental source: strain O157:H7, substrain RIMD 0509952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
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                                                                      R; Ishikawa, K.; Nagase, T
DNA Res. 5, 169-176, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:Q9R396; UNIPARC:UPI00000D00CA; GB:AE005174; NID:g12518449; A;Experimental source: strain O157:H7, substrain EDL933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
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                                                                                          Kotani, H.;
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VPPAPPMPIVTDG

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A;Molecule type: mRNA
A;Residues: 1-968 <ISH>
A;Cross-references: UNIPROT:075179; UNIPARC:UPI000017C1C1; EMBL:AB014597; NID:g3327207;
A;Experimental source: brain; clone HK04486
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                             RESULT 5
T24955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
T20369
                                                                                                                                                                                                                                  submitted to the EMBL Data Library, A;Reference number: Z19960 A;Accession: T24955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-1026 <WIL>
A;Cross references: UNIPROT:Q18987;
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S
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                                                                                                                                                         A;Cross references: UNIPROT:Q9XUP5;
A:Experimental source: clone T16G1
                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                   R;Lloyd,
                                                                                                                                                                                                                                                                                                hypothetical protein T16G1.8 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T24955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: CESP:D2045.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein D2045.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 09-Jul-2004 C;Accession: T20369
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                                                                                                            A; Map position:
                                                                                                                         A; Gene: CESP:T16G1.8
                                                                                                                                                                                       A; Residues: 1-365 <WIL>
                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
                              Query Match
Best Local S
Matches 9
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12; Conserv
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 IPPAPPLPSOTDG 27
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                                             Score 57;
Pred. No.
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Pred. No. 15;
5; Mismatches
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Pred. No.
                             Pred. No. 7.4
                                                                                                                                                                                                                                                                   November
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UNIPARC: UPI000004E81F;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          August 1994
                                                                                                                                                                        UNIPARC: UPI0000076820; EMBL: Z81592;
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                                                               Length 365;
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                                  Indels
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                                                                                                                                                                           PIDN: CAB04730.1;
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RESULT
C75162
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C;Keywords: transmembrane protein
F;7-23/Domain: transmembrane #status predicted <TMl>
F;445-461/Domain: transmembrane #status predicted <TM2>
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A;Residues: 1-487 <DEL>
A;Cross-references: UNIPARC:UPI000006C2C8; EMBL:Z73633; NID:g1370569; PID:e246983; PID:
A:Fxnerimental source: strain S288C (AB972)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: S65310; S65331

R;Duesterhoeft, A.; Floeth, M.; Fritz, M.; Hilbert, H.; Moestl, submitted to the Protein Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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3-phosphoshikimate 1-carboxyvinyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N;Alternate names: hypothetical protein P0318 C;Species: Saccharomyces cerevisiae
                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: SGD:S0006198
                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable membrane protein YPL277c - yeast (Saccharomyces cerevisiae)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introns: 54/2;
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A; Residues: 1-631 < CLA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Clarke,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T12F5.5 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              );Reference number: S65292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Reference number: S64967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;Cross-references: UNIPROT:Q08989; UNIPARC:UPI000006C2C8; Experimental source: strain S288C (AB972)
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                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Accession: S6533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Date: 10-Dec-1994 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
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Best Local
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                                                                                                       GREGNGTNGDHPKGPPPPPPPPPEKG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
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Pred. No. 14;
4; Mismatches
                                                                                                                                                                                                        Score 56.5;
Pred. No. 1
                                                                                                                                                                                     Mismatches
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14;
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  (aroa) PAB0306 -
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Pyrococcus abyssi (strain
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A;Residues: 1-1420 - OLI>
A;Cross-references: UNIPROT:013736; UNIPARC:UPI0000069639; EMBL:Z98529; PIDN:CAB11030.1;
A;Experimental source: strain 972h-; cosmid c16E8
C;Genetics:
                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
                                                                                                                    R;Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, submitted to the EMBL Data Library, September 1995
A;Reference number Z21746
A;Accession: T37781
                                                                                                                                                                             C;Accession: T37781
R;Oliver, K.; Harri
                                                                                                                                                                                                              probable cytoskeleton assembly control protein - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                RESULT 10
T37781
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R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, Lory, S.; Olson, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: A82950; MUID:20437337; PMID:10984043 A;Accession: F83015
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C;Superfamily: 3-phosphoshikimate 1-carboxyvinyltransferase; 3-phosphoshikimate 1-carbo:
F;19-401/Domain: 3-phosphoshikimate 1-carboxyvinyltransferase homology <PSK>
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submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: PA5037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-551 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein PA5037 [imported] - Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F83015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: A75001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Pyrococcus abyssi
                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Pseudomonas aeruginosa
Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cross-references: UNIPROT:Q9HUD4; Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                              PIGNLGNN-VNGNHLIPPAP-----PLPSQTDGAA
                                                                                                                                                                                                                                                                                                                                                       PVTPLANNGVTPMHPVPPAPTEPTAPAATPTPTQTPAPA 408
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genome sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 56;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          UNIPARC: UPI00000C5EDA; GB:AE004917; GB:AE004091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNIPARC: UPI0000034469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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A.; Larbig,
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A;Molecule type: DNA
A;Residues: 1-624 <DEL>
A;Residues: 10-624 <DEL>
A;Cross-references: UNIPROT:Q08912; UNIPARC:UPI000006C43D; EMBL:275297; NID:g1420836;
A;Experimental source: strain S288C
R;Duesterhoeft, A.; Floeth, M.; Fritz, M.; Hilbert, H.; Moestl, D.
                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S67301; S65311; S65332
R;Delius, H.; Hebling, U.; Hofmann, B.
submitted to the Protein Sequence Database, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      probable membrane protein YOR389w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein 06780; hypothetical protein P0315
C;Species: Saccharomyces cerevisiae
C;Date: 12-Jul-1996 #sequence_revision 12-Jul-1996 #text_change 09-Jul-2004
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A;Map position: 1
A;Introns: 78/3
                 R;Delius, H.; Hebling, U. submitted to the Protein Sequence Database,
                                                 A;Molecule type: DNA
A;Residues: 525-624 GUE>
A;Residues: 525-624 GUE>
A;Cross-references: UNIPARC:UPI000006A4CB; EMBL:Z73634; NID:g1370571; PID:e246984;
A;Experimental source: strain S288C (AB972)
                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S67261
A; Accession: S67301
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A;Contents: annotation; possible protein-coding frames
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P28955; UNIPARC:UPI0000136B9F; GB:M86664; NID:g330791; PIDN R;Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J. Virology 189, 304-316, 1992
A;Title: The DNA sequence of equine herpesvirus-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Telford, E.A.R.; Watson, M.S.; McBride, K.; Davison, A.J. submitted to GenBank, March 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: equine herpesvirus 1
A;Note: host Equus caballus (domestic horse)
C;Date: 30-Sep-1992 #sequence_revision 30-Se
                                                                                                                                                                   A; Accession: S65311
                                                                                                                                                                                                          submitted to the Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Description: The DNA sequence of equine herpesvirus-1
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                                                                                                                                                                                         A; Reference number: S65292
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  number:
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Pred. No.
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Pred. No.
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1.3e+02;
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A; Map position:
                      A; Gene: CESP: C35E7.2
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Genetics:

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C;Accession: T48170
R;Bevan, M.; Terryn, N.; Ardiles,
ewes, H.W.; Rudd, S.; Lemcke, K.;
submitted to the Protein Sequence
A;Reference number: Z24487
A;Accession: T48170
                                                                                                                          R;Graves, T.; MCDONALW, A. submitted to the EMBL Data Library, May 1998 near-intion: The sequence of C. elegans co
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T48170
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Mosldues: 1-687 <GRA>
A;Residues: 1-687 <GRA>
A;Cross-references: UNIPARC:UPI0000179ED6; EMBL:AF067216; PIDN:AAC17518.1; GSPDB:GN00019
A;Experimental source: strain Bristol N2; clone C35E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ca2+/H+ exchanger-like protein - Arabidopsis thal N;Alternate names: protein F7A7.10 C;Species: Arabidopsis thaliana (mouse-ear cress)
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A;Residues: 525-624 <DE2>
A;Residues: 525-624 <DE2>
A;Cross-references: UNIPARC:UPI000006A4CB; EMBL:Z73634; NID:gl370571; PID:e246984; PID:g
A;Experimental source: strain S288C (AB972)
                                                                                           A; Reference number: Z21278
A; Accession: T33077
                                                                                                                                                                                          C; Accession: T33077
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A;Experimental source: cultivar Columbia; BAC clone F7A7
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A; Residues: 1-442 <BEV>
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C; Keywords: transmembrane protein
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Best Local Similarity
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9; Conserva
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ilarity 44.0%;
Conservative
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Pred. No.
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Database, March 2000
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Pred. No. 2
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17;
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C;Specie
C;Date:
                                                        RESULT 17
T28914
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A; Molecule type: DNA
A; Residues: 1-262 < JOR>
A; Cross-references: UNIPROT:Q9LXW0; UNIPARC:UPI00000AAB06;
A; Cross-references: cultivar Columbia; BAC clone T15B3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein T15B3.140 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
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T18289
     hypothetical protein T26C11.1 - C. C; Species: Caenorhabditis elegans C; Date: 29-Oct-1999 #sequence_rev
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C;Genetics:
A;Gene: racGAP
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A; Title: Cloning of a rhoGAP homolog from Dictyostelium A; Reference number: Z18858; MUID:97332648; PMID:9188459 A; Accession: T18289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             racGAP protein - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18289
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A; Residues: 1-1335 <
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R;Ludbrook, S.B.; Eccleston,
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Best Local Similarity
Matches 12; Conserv
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Best Local
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#sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
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                                    Caenorhabditis elegans
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Pred. No. 60;
2; Mismatches
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Pred. No. 11;
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Pred. No. 28;
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Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome see
A;Reference number: A82950;
A;Accession: A83422
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R;Stover, C.K.; Pham, X.Q.;
adman, S.; Yuan, Y.; Brody,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: BMEII0694
A;Map position: II
C;Keywords: oxidoreductase
                                                                                                                                                                                                       hypothetical protein PA1797 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa C;Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella meliten.
A; Molecule type: DNA
A; Residues: 1-610 <STO>
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                                    A; Status: preliminary
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A;Experimental source: strain 16M
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A; Residues: 1-452 < KUR>
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C; Accession: AE3596
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C;Species: Brucella melitensis
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A; Residues: 1-233 <MAR>
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A;Accession: T28914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78/3; 126/3
                                                                           sequence of Pseudomonas aeruginosa PAO1, 50; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.7%;
                                                                                                                                                    Erwin, A.L.; Mizoguchi, L.L.; Coulter, S.N.; Fo.
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Pred. No. 11;
0; Mismatches
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No:
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23;
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Folger, K
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                                                                                                                                                      K.R.;
                                                                                                                                                  K.R.; Kas,
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A.; Larbig,
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                                                                                                                                                    M.J.;
K.; Li
                                                                                             pathc
                                                                                                                                                    Lim,
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Cross-references: UNIPROT:Q912U5; UNIPARC:UPI00000C54A1; GB:AE004605; GB:AE004091; NID

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RESULT 22
A83412
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                                                                                                                                                                                                                                                             A; Cross-references: UNIPARC: UPI000017B7C2;
A; Cross-references: UNIPARC: UPI000017B7C2;
                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein C25H3.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T15624
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: CESP:F14D12.1
A;Introns: 5/3; 28/3; 113/3; 155/2; 226/1; 260/1; 298/2; 363/3; 462/3; 509/1; 567/2; C;Superfamily: Caenorhabditis elegans hypothetical protein F14D12.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-645 <MIN>
A;Cross-references: UNIPARC:UPI00001793D0; EMBL:U41021; NID:g1086679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid F14D12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F14D12.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep_1999 #sequence_revision 20-Sep_1999 #text_change 04-Mar-2000 C;Accession: T16078
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                                                                       밁
                                                                                                                                                                                             A;Gene: CESP:C25H3.b
A;Introns: 58/1; 213/3; 273/1; 446/2; 468/2; 484/2; 510/1; 552/1; 609/1
                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                   A; Reference number: Z18379
A; Accession: T15624
                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, June 1995 A;Description: The sequence of C. elegans cosmid C25H3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Reference number: Z18457
A;Accession: T16078
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 21
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Gene: CES
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Best Local :
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                                                                     610 IENAGNEIVQVHLGPLSPPITDQTE 634
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10; Conserv
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ilarity 55.6%;
Conservative
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44.0%;
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47.6%;
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; Pred. No. 35;
4; Mismatches
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Pred. No.
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Pred. No.
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35;
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33;
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                  A;Cross-references: UNIPROT:Q9CBD6; UNIPARC:UPI00000C6E3D; GB:AL450380; NID:g13093715;
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R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.; eam, M.A.; Rutherford, K.M. Mature 409, 1007-1011, 2001
A;Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, A;Title: Massive gene decay in the leprosy bacillus. A;Reference number: A86909; MUID:21128732; PMID:11234002
A;Accession: B87180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein [imported] - Staphylococcus aureus (fragment)
C;Species: Staphylococcus aureus
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 11-May-2000
C;Accession: T44106
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A;Molecule type: DNA
A;Residues: 1-2468 <STO>
A;Cross-references: UNIPROT:Q912M3; UNIPARC:UPI00000C54E3; GB:AE004613; GB:AE004091; NID
A;Cross-references: UNIPROT:Q912M3; UNIPARC:UPI00000C54E3; GB:AE004613; GB:AE004091; NID
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Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, ar A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83412
                                                                                                                                                                                                                                          C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change
C;Accession: B87180
                                                                                                                                                                                                                                                                                   pyruvate (or indolepyruvate) decarboxylase [imported] - Mycobacterium leprae C_iSpecies: Mycobacterium leprae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antimicrob. Agents Chemother. 43, 1449-1458, 1999
A;Title: Cloning and nucleotide sequence determination of the A;Reference number: Z22733; MUID:99278010; PMID:10348769
A;Accession: T44106
A; Molecule type: DNA
A; Residues: 1-569 <STO>
                                             A;Status: preliminary
                                                                                                                                                                                             R;Cole, S.T.; Eiglmeier, K.; Parkhill, J.; James, K.D.; R.; Davies, R.M.; Devlin, K.; Duthoy, S.; Feltwell, T.;
                                                                                                                                                                                                                                                                                                                                  B87180
                                                                                                                                                                                                                                                                                                                                                     RESULT 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: strain N315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPARC:UPI000017AC12; EMBL:D86934; PIDN:BAA82208.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene:
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C;Species: Pseudomonas aeruginosa
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Best Local
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ilarity 50.0%;
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Pred. No. 12;
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Pred. No. 1.7e+02;
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                                                                                          PMID:11234002
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                                                                                                                                     Skelton,
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Larbig,
                                                                                                                                     Squares,
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K.; Lim,
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                                                                                                                                                                                                                                                                                                                                                              R;Schulte, U.; Aign, V.; submitted to the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Neurospora crassa
C;Date: 21-Jul-2000 #sequenc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            related to C2H2 zinc finger transcription N; Alternate names: protein B7F21.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:O64825; UNIPARC:UPI0000048575; EMBL:AC004482; NID:g3152602; R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; R;Lin, X.; Woffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. ems. Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. ems. D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Vandard, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Vandard, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Vandard, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Vandard, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Vandard, D.; Vandard, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Vandard, D.; Vandard, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Vandard, D.; Vandard, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Vandard, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Vandard, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Vandard, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Vandard, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Vandard, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Vandard, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Vandard, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Vandard, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Vandard, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Vandard, W.C.; White, O.; Eisen, J.A.; Salzberg, W.C.; White, O.; Eisen, W.C.; White, O.; Ei
                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-770 <SCH>
                                                                                                                                                                                                                                                                 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                               A; Reference number: Z25286
                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: T51024
                                                                                                                                  A; Experimental
                                                                                                                                                                                                                                                                                                    A; Accession: T51024
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R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Rsubmitted to the EMBL Data Library, May 1998
A;Description: Arabidopsis thaliana chromosome II BAC F2714 genomic sequence.
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C;Superfamily: pyruvate
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N,Alternate names: protein kinase homolog F27L4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches
      ;Map position:
;Introns: 117/1
                                                                    Gene: NCSP:B7F21.50
                                                                                                                                                              Cross-references: UNIPROT: Q9P319; UNIPARC: UPI000017B4E0;
                                                                                                       Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene: F27L4.5; At2g23770
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                                                                                                                                      source:
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64.3%;
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Colway, A.B.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Colway, A.B.; Chin, C.W.; Chung, M.K.; Chuzar, L.

Nature 408, 816-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A; Title: Sequence and analysis of Chromosome 1 of the plant Arah

A; Title: Sequence and analysis of Chromosome 1 of the plant Arah
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A;Authors: Parry, C:; Quail, M:; Rutherford, K:; Simmonds, M:;
A;Title: Complete genome sequence of a multiple drug resistant

A;Title: Complete genome sequence of a multiple drug resistant

A;Title: AB0502; MUID:21534947; PMID:11677608
                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q9C8B9; C;Genetics:
                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-302 <STO>
                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A86141; A; Accession: C86480
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C86480
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                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.2K hypothetical protein - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 C;Accession: C86480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-276 < PAR>
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NLGNN-----VNGNHLIPPAPPLP 22
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P.; Cronin, A.; Davis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNIPARC: UPI000005A0A0; GB:AL513382; PIDN: CAD05333.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J.R.; Palm,
                                                                                      31.5%;
44.0%;
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                                                                                                                                                                                                                                                                 UNIPARC: UPI00000A8A47; GB: AE005172; NID: g11055830;
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                                                                  Mismatches
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                                                                                                 26;
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Salmonella enterica serov
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.S.; Maiti,
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R;anonymous, The C. elegans Sequencing Consortium.

Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog A;Reference number: A75000; MUID:99069613; EMID:9951916
A;Note: see websites genome wistl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_elegans/Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: E88633
A;Reference number: Z15455
A;Accession: T05865
A;Molecule type: DNA
                                                                hypothetical protein T29A15.90 - Arabidopsis thaliana (;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004 C;Accession: T05865 R;Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Volcl submitted to the Protein Sequence Database, March 1999
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Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 199
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C;Species: Caenorhabditis elegans
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C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
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E88633
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A; Residues: 1-382 <STO>
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                                                                                                                                                                                                             T05865
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1; Mismatches
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hypothetical protein M04G12.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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T49833
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C;Species: Neurospora crassa
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A; Introns: 65/3; 153/2; 192/3; 262/2
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                                                                  A; Introns: 193/3; 458/1; 505/3; 553/2
                                                                                  A; Map position:
                                                                                                    A;Gene: CESP:M04G12.4
                                                                                                                                  A;Residues: 1-561 <WIL>
A;Cross-references: UNIPROT:P92007; UNIPARC:UPI000016426E;
A;Experimental source: clone M04G12
                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                    A; Reference number: Z19789
A; Accession: T23722
                                                                                                                                                                                                                                                      submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                       R;Sims,
                                                                                                                                                                                                                                                                                       C; Accession: T23722
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A; Introns: 56/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q9P526; UNIPARC:UPI00000695C4; EMBL:AL356815; GSPDB:GN00116; A;Experimental source: BAC clone B24H17; strain OR74A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-554 < SCH>
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C; Accession: T49833
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                                                                                                                                                                                     A; Molecule type: DNA
                   Query Match
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Similarity 9; Conserv
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                 31.5%; Score 52; 47.4%; Pred. No.
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Database, Ma
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Pred. No. 53;
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                                   Length 561;
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Submitted to the EMBL Data submitted to the EMBL Data
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A;Description: Sequence analysis of a 3.5 Mb contig in human 19p13.3 containing a serine A;Reference number: Z14157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004 ():Accession: T00492
R;Lamerdin, J.E.; McCready, P.M.; Skowronski, E.; Adamson, A.W.; Burkhart-S.; Christensen, M.; Georgescu, A.; Avila, J.; Liu, S.; Attix, C.; Andreise, Arellano, A.; Montgomery, M.; Ow, D.; Nolan, M.; Trong, S.; Kobayashi, A.; Arellano, A.; Montgomery, M.; Ow, D.; Nolan, M.; Trong, S.; Kobayashi, A.;
                                     A; Reference number:
A; Accession: T22685
                                                                                                                          hypothetical protein F55A11.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct-1999 #te:C;Accession: T22685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, November 1995 A;Description: The sequence of C. elegans cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-725 < LAM>
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;Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Z18365
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                   translated from GB/EMBL/DDBJ
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Pred. No.
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Pred. No. 15;
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                                                                               May 1996
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Liu, S.; Attix, C.; Andreise, T.; Tr:
M.; Trong, S.; Kobayashi, A.; Olsen, I
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                                                       A;Cross-references: UNIPROT:Q96UB6; UNIPARC:UPI000017B44B; A;Experimental source: cosmid contig 68B2; strain 74
                                                                                                 A; Molecule type: DNA
A; Residues: 1-503 <SCH>
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               Gene: NCSP:68B2.90
                                     Genetics:
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preliminary

EMBL:AL353821; GSPDB:GN00112

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R;Schulte, U.; Aign, V.; Hoheisel, submitted to the Protein Sequence
                                                                                  C;Species: Neurospora crassa
C;Date: 05-May-2000 #sequenc
C;Accession: T48825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Nolecule type: DNA
A; Molecule type: DNA
A; Residues: 135-141, 'I',143-173,'S',175-257,'E',259-274 <MEN>
A; Residues: 135-141, 'I',143-173,'S',175-257,'E',259-274 <MEN>
A; Cross-references: UNIPARC: UPI000010EC69; GB:L01464; NID:g332105; PIDN:AAA46538.1;
A; Cross-reference extracted from NCBI backbone (NCBIN:119080, NCBIP:119081)
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A;Cross-references: UNII
A;Experimental source: (C;Genetics:
A; Reference number: Z24541
A; Accession: T48825
                                                                                                                                                                                                                                                                                                                                                                                                                        C; Keywords: a F; 185/Active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Menendez-Arias, L.; Young, M.; Oroszlan, S.
J. Biol. Chem. 267, 24134-24139, 1992
A;Title: Purification and characterization of the mouse mammary tumor virus A;Reference number: A45125; MUID:93054787; PMID:1331110-A;Accession: A45125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Complete nucleotide sequence of a milk-transmitted A;Reference number: A93030; MUID:87112944; PMID:3027377 A;Accession: B26795
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R;Moore, R.; Dixon, M.; Smi
J. Virol. 61, 480-490, 1987
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PRMVMM
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C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change
                                                                                                                                              hypothetical protein 68B2.90 [imported] - Neurospora crassa
                                                                                                                                                                      T48825
                                                                                                                                                                                         RESULT
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A; Residues: 1-274 < MOO>
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                                                                                                                                                                                                                                                                                                                                                                                                                 ;Complex: homodimer
;Keywords: aspartic proteinase; homodimer;
;185/Active site: Asp (shared with dimeric
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                              B.; Holland; R.;
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A;Molecule type: mRNA
A;Residues: 1-346 <AAA>
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A;Accession: T46916
                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
C;Accession: T46916
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F;333-349/Domain: transmembrane #status predicted <TMM>
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A;Residues: 1-612 <RIE>
A;Residues: 1-612 <RIE>
A;Cross-references: UNIPARC:UPI000013BD4C; EMBL:Z73540; NID:g1370385; PID:e246913; PID:
A;Experimental source: strain S288C (AB972)
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A;Residues: 1-612 <BEN>
A;Residues: GNIPROT:Q08925; UNIPARC:UPI000013BD4C; EMBL:Z73540; NID:g1370385; PI
A;Experimental source: strain S288C (AB972)
A;Experimental source: Strain S288C (AB972)
R;Rieger, M.; Mueller-Auer, S.; Schaefer, M.
Submitted to the Protein Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: S65196; S65203

R;Benes, V.; Rechmann, S.; Nentwich, U.; Voss, H.; Ansorge, W. submitted to the Protein Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable membrane protein YPL184c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein P2221
C;Species: Saccharomyces cerevisiae
C;Date: 10-Dec-1994 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
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A;Map position: 16L
C;Keywords: transmembrane protein
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                                                                                                                                                   A; Note: DKFZp762E117.1
                                                                                                                                                                                      A;Cross-references: UNIPROT:Q9NSQ9; UNIPARC:UPI0000071125; EMBL:AL157480
A;Experimental source: adult melanoma (MeWo cell line); clone DKrZp762E117
                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein DKFZp762E117.1 - human (fragment)
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A;Accession: S65203
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                                                                                     30.9%;
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44.0%; Pred. No. 69;
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Pred. No. 55;
3; Mismatches
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Db 225 VSGSRSSPPAPPLP 238

Search completed: August 1, 2006, 21:47:25 Job time : 45 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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               Score
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Copyright (c) 1993 - 2006
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Biocceleration Ltd.
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ABU72001	ABR78381	ABO18960	ABR92319	ABO16419	ABR98896	ABR99506	ABO33984	ABU90925	ABU80588	ABU67560	ABU86347	ABU89506	ABU91813	ABU98107	ABU98892	ABU85732	ABR94759	ABR74997	ABO02843	ABO08791	ABU92714	
Abu72001	Abr78381	Abo18960	Abr92319	Abo16419	Abr98896	Abr99506	Abo33984	Abu90925	Abu80588	Abu67560	Abu86347	Abu89506	Abu91813	Abu98107	Abu98892	Abu85732	Abr94759	Abr74997	Abo02843	Abo08791	Abu92714	
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ALIGNMENTS

RESULT 1 ADC00799 ID ADC00 AC ADC0 AC ADC0 AX ADC0 AX Ente XX ente XX ente XX Esch XX 10-D XX 10-D XX (UYI XX (UYI XX Ente PH and XX Ente PH and XX The CC O157 CC has CC genc CC genc CC genc CC sequ 24-JAN-2002; 2002JP-00015959. JP2002355074-A. Escherichia coli; 0157:H7. 10-DEC-2002. enterohaemorragic; anti-bacterial. Enterohaemorragic E. coli 0157:H7-specific protein SEQ ID NO: 844 04-DEC-2003 ADC00799; ADC00799 standard; protein; (first entry) 558 ₿

Enterohemorragic Escherichia coli O157:H7-specific nucleic acid molecule and a polypeptide and its use, a polypeptide, a vector and a host cell. WPI; 2003-451640/43. 24-JAN-2001; 2001JP-00112010. (UYTS-) UNIV TSUKUBA.

The invention relates to a novel enterohaemorragic Escherichia coli 0157:H7-specific nucleic acid molecule. A polynucleotide of the invention has anti-bacterial activity. The polypeptide can be used in detection and/or treatment of 0157:H7 infection. The nucleotide sequence of the genome of Enterohaemorragic E coli 0157:H7 was determined. The present sequence represents an E. coli 0157:H7-specific polypeptide of the Sequence 558 Claim 3; SEQ ID NO 844; 2067pp; Japanese.

5 Query Match
Best Local Similarity
Matches 558; Conserv MPIGNLGHNPNVNNSIPPAPPLPSQTDGAGGRGQLINSTGPLGSRALFTPVRNSMADSGD 100.0%; Score 2840; DB 7; ilarity 100.0%; Pred. No. 1.7e-193; Conservative 0; Mismatches 0; Length 558; 0, Gaps 60

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RESULT 2
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                                                                                                                                                                                                                                                                                                                         Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                algorithm; adhesin; pharmaceutical; vaccine; drug screening;
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2004US-0589227P.
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comprises computing sequence-based attributes of protein sequences using neural network software and training an artificial neural network.

Claim 16; SEQ ID NO 20; 402pp; English.

CC identifying adhesin and adhesin-like proteins, by computing the sequenceCC based attributes of protein sequences using five attribute modules of a
CC each of the computed five attributes, and identifying the adhesin and
CC each of the computed five attributes, and identifying the adhesin and
CC edhesin-like proteins having probability of being an adhesin (Pad) as
CC equal or greater than 0.51. Also claimed is a set of 1274 annotated genes
CC encoding adhesin and adhesin-like proteins, having 274 fully defined 162CC 11151 base pair (SEQ ID NO: 385-658) sequences; a set of 105 hypothetical
CC genes encoding adhesin and adhesin-like proteins, having 105 fully
CC defined 306-15876 base pairs (SEQ ID NO: 659-763); a set of 1279 annotated
CC adhesin and adhesin-like proteins, having 279 fully defined 53-3716 base
CC pair (SEQ ID NO: 1-279); a set of 105 hypothetical adhesin and adhesin-like proteins, having 279 fully defined 53-3716 base
CC 280-384) sequences; and a fully connected multilayer feed forward ANN (I)
CC based on (MI). (MI) is useful for identifying adhesin and adhesin-like
CC proteins for further testing in development of new vaccine formulations
CC useful for identifying putative adhesins that are important in drug
CC discovery and preventing therapeutics for whooping cough, pneumonia,
CC gastric ulcer and urinary tract infections. (MI) identifies adhesins from
CC unique proteins. The present sequence is a microbial pathogen adhesin
CC unique proteins. The present sequence is a microbial pathogen adhesin

Sequence 558 AA;

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                NMGNTDSVVYSTIQHPPRDTTDNGARLLGNPSAGIQSTYARLALSGGLRHDMGGLTGGSN
                                                                                NVDTPGSEDTMESRRSSMASTSSTFFDTSSIGTVQNPYADVKTSLHDSQVPTSNSNTSVQ
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NMGNTDSVVYSTIQHPPRDTTDNGARLLGNPSAGIQSTYARLALSGGLRHDMGGLTGGSN
                                                               NVDTPGSEDTMESRRSSMASTSSTFFDTSSIGTVQNPYADVKTSLHDSQVPTSNSNTSVQ
                                                                                                                           AGYGLSGALILGGGIGVAVTAALHRKNQPVEQTTTTTTTTTTTSARTVENKPANNTPAQG
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Pred. No. 1.7e-193;
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RESULT 3
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                                                                                                                                                                                       The present invention relates to novel EspFU polypeptides and their corresponding polymucleotides. The EspFU polypeptides are EspF-like CC corresponding polymucleotides. The EspFU polypeptides are EspF-like CC polypeptides encoded by genes of the cryptic prophage CP-933U of CC coli (EPEC) that binds to a neuronal wiskott-aldrich syndrome protein (N-CC wasp) polypeptide or restores the actin pedestal formation activity of CC enteropathogenic E. coli (EPEC) strain KC12. The invention further CC relates to a method of identifying a candidate compounds capable of CC binding to and/or modulating the activity of EspFU and compounds that CC inhibits protein-protein interactions between EspFU and EspFU-interacting proteins such as N-WASP, transducer of Cdc42-dependent actin assembly-1 CC (Toca-1) and p21-activated kinase 1 (Pakl). EspFU polymucleotides are CC useful for treating BHEC infection. The present sequence is the CC enterohemorrhagic Escherichia coli translocated intimin receptor (Tir) circum. This sequence is critical for the formation of actin pedestals
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Best Local Similarity
Matches 558; Conser
                                                                                                                                                        Sequence 558 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 12; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel purified polypeptide having six residues of EspF-U, and binding neuronal Wiskott-Aldrich syndrome protein polypeptide, useful for identifying EspF-U activity modulating compound.
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N-PSDB; AEE86219.
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(CAMP/) CAMPELLONE K G.
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100.0%; Pr
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                                                                                                Score 2840; DB 10;
Pred. No. 1.7e-193;
; Mismatches 0;
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RESULT 4
AAYO6221
ID AAYO
XX AAYO
AC AAYO
AC AAYO
AC AAYO
DT 16-A
XX Tir;
KW Tir;
KW Infe
XX Esch
XX INFE
YF Misc
FT New
PR N-PS
XX New
PT New
P
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                          New translocated intimin receptor useful for treating infection enteropathogenic or enterohemorrhagic Escherichia coli.
                                                                                                              WPI; 1999-337712/28
N-PSDB; AAX58859.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                  Finlay
                                                                                                                                                                                                                                                                                                                 12-NOV-1997;
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                                                                                                                                                                                                                                                           (UYBR-) UNIV BRITISH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          translocated intimin receptor; Hp90; enterohaemorrhagic; EHEC;
ction; diagnosis; vaccine.
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                                                                                                                                                                                                  BB,
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                       enterohemorrhagic Escherichia coli
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                                                       RESULT 5
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                                                                                                                                                                                                     -GNTDSVVYSTIQHPPRDTTDNGARLLGNPSAGIQSTYARLALSGGLRHDMGGLT
                  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.4%;
94.0%;
                    549
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 2624.5; DB 2
Pred. No. 3.8e-178;
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                    A
                                                                                                          559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               559;
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Ş 멍 5

59

Query Match Best Local S Matches 328

Similarity

56.4%;

Conservative

60;

Score 1534.5; DB 2 Pred. No. 1.6e-100; 0; Mismatches 137;

Indels Length

57;

Gaps

11

58 60

DB 2;

549;

MPIGNLGHNENVNNSIPPAPPLPSQTDGA--GGRGQLINSTGPLGSRALFTPVRNSMADS

GDNRASDVPGLPVNPMRLAA--SEITLNDGFEVLHDHGPLDTLNRQIGSSVFRVETQEDG MPIGNLGNNVNGNHLIPPAPPLPSQTDGAARGGTGHLISSTGALGSRSLFSPLRNSMADS

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The present sequence represents Tir, a novel translocated intimin CC (EPEC) strain. The sequence was deduced from an isolated tir CC (EPEC) strain. The sequence was deduced from an isolated tir CC (EPEC) strain. The sequence was deduced from an isolated tir CC polynucleotide (see AAX58858). Tir proteins are secreted by attaching and CC effacing pathogens such as EPEC and EHEC (see AAY06221) E. coli. The CC surfaces, to which the pathogen then adheres to trigger additional host CC signaling events and actin nucleation. Diagnosis of disease caused by CP pathogenic E. coli can be performed by use of antibodies that bind to Tir CC to detect the protein or the use of nucleic acid probes for detection of CC nucleic acids encoding Tir polypeptide. Isolated Tir nucleic acids, Tir peptides, a recombinant method for producing recombinant Tir, antibodies which bind to Tir, and a kit for the detection of Tir-producing E. coli care provided. A method of immunising a host with Tir to induce a proteins can be used in attenuated E. coli to induce a cell-mediated CC immune response to other polypeptides, e.g. antigens. A method for compounds which interfere with the binding of bacterial CC pathogens to their receptors is further provided
                                                                                                                                                                                                                                                                                                                                                                                    New translocated intimin receptor useful for treating infection enteropathogenic or enterohemorrhagic Escherichia coli.
Sequence
                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPEC E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-337712/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 W09924576-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tir; translocated intimin receptor; Hp90; enteropathogenic; EPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-AUG-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UYBR-) UNIV BRITISH
                                                                                                                                                                                                                                                                                                                                                      6; Page 55-58; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coli translocated intimin receptor (Tir)
549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis;
A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "given as Xaa in the specification;
from the DNA sequence"
364. .386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "putative transmembrane domain'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Devinney
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                                             Claim 8; Page 76; 96pp; English.
                                                                                              Screening for inhibitors of intimin binding to eukaryotic cells, for use in diagnosing, preventing and treating bacterial infections, especially Escherichia coli O157:H7.
                                                                                                                                                                                                         WPI; 2000-499357/44.
                                                                                                                                                                                                                                                                                                                                                             29-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                             31-JAN-2000; 2000WO-GB000254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diarrhoea; antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Intimin; Tir binding domain; inhibitor; Tir-independent eukaryotic cell binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB20576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB20576 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Intimin C-terminal Tir binding domain amino acid sequence
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                                                                                                                                                                                                                                                       GM, Matthews
                                                                                                                                                                                                                                                                                                          IMPERIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         activity; bacterial infection;
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                                                                                                                                                                                                                                                       G
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present invention describes a

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling

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Best Local :
                                                                                     New isolated nucleic acid genes from Drosophila and interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 infections cause a histopathological effect known as attachment and effacement on intestinal epithelial cells. The inhibitors can be used to produce food supplements or additives, especially where the food is a milk substitute. The method can be used to sort cells based on their ability to bind to a Tir independent cell binding domain of an intimin polypeptide. Polypeptides having Tir-independent intimin binding activity can be used to produce a vaccine against a bacterial disease. The present sequence represents a specifically claimed intimin C-terminal Tir binding domain amino acid sequence, for use in the method of the present
                                                     Disclosure; SEQ ID NO 31017; 21pp + Sequence Listing; English
                                                                                                                                                  N-PSDB;
                                                                                                                                                                                              Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         intimin binding to eukaryotic cells. The method comprises exposing an intimin polypeptide having a Tir-independent cell binding activity to test agents, and obtaining an inhibitor based on its ability to bind the polypeptide. The inhibitors are used in the prevention, treatment and/or diagnosis of bacterial infections, preferably by enteropathic and/or enterohaemorrhagic Escherichia coli, Shiga toxigenic E. coli, Hafnia alvei or Citrobacter freundii, or especially E. coli 0157:H7. The
                                                                                                                                                                                                                                                        23-MAR-2000; 2000US-0191637P
11-JUL-2000; 2000US-00614150
                                                                                                                                                                                                                                                                                                       23-MAR-2001; 2001WO-US009231
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                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                    pharmaceutical.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB68075;
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                                                                                                                                                                                                                           (PEKE ) PE
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Pred. No. 4.4e-21;
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Best Local Similarity
Matches 130; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
Drosophila melanogaster
                                             Drosophila; developmental biology; cell
                                                                                                            26-MAR-2002
                                                                                                                                                                       ABB66878 standard; protein; 2586
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                                                                                                                                                                                                                                                                                                                                                                                                             IGTVQ-----NPYADVKTSLHDSQVPTSNSNTSVQNMGNTDSVVYSTIQH------
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                                                                                                                                                                                                                                                                                                                 LAAAQSIHCEALGGFPTGSTGSQRKRAQAGEPTTSCSSTTISNVEPLLKTPERRLKLTLR
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                                                                         melanogaster polypeptide SEQ
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No. 0.00047;
                                            signalling; insecticide;
                                                                             ID NO 27426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     245; Indels 188;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO
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genes from Drosophila
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11-JUL-2000;
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les 113; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to an isolated nucleic acid detection reagent able of detecting 1000 or more genes from Drosophila. The invent
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DB; ABL10981.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNLGHNPNVNNSIPPAPPLP----SQTDGAGGRGQLIN----STGPLGSRALFTPVR
PYADV---KTSLHDSQVPTSNSNTSVQNMGNTDSVVYSTIQHPPRDTTD--NGARLLGNP
                                                                                                                                                                              RDQLTKEAFQNPDNQKVNIDELGNAIPSGVLKDDVVANIEEQAKAAGEEAKQQAIENNAQ
                                                                                                                                                                                                            EGQTTSSSDPVVEVAQGSSSNG----
                                                                                                                                                                                                                                          ---SSLRSDPKLWLALGTVATGLIGLAATGIVQALALTPEPDSPTTTDPDAAASATETAT
                                                                                                                                                                                                                                                                       TTTTTTS---
                                                                                                                                                                                                                                                                                                  VASDITEARQRILELLEPKGTGESKGAGESKGVGELRESNSGAENTTETQTSTST-----
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                             TTTTTTSSDGGQSTTSSDPVVEVSQGTNGGN---SSTQSSSATTTTTSSDEGQTTSSSD
                                                                                       TOSSSSTTTTTSSDEGOTTSSSDPVGEVAQGSSSNGDGNST---
                                                                                                                   AQKKYDEQQAKRQEELKVSSGA----GYGLSGALILGGGIGVAVTAALHRKNQPVEQTTTT
                                                                                                                                                  TTTTSSDGGQ---
                                                                                                                                                                                                                                                                                                                              QSSS-----STTTTTSSDEGQTTSSSDPVVEVAQGSS----SNGDGNSTQSLTT
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                                                         TTTTTTTSARTVENKPANNTPAQGNVDTPGSEDTMESRRSSMASTSSTFFDTSSIGTVQN
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2000US-00614150
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19.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 182.5; DB 4;
Pred. No. 0.0025;
5; Mismatches 237;
                                                                                                                                                                                                                                                                    SDGGQSTTSSDPVVEVSQGTNGGNSSTQSSSSTTTTTSSD
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18-NOV-1998;
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Pan J, I
Williams
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15-MAR-2000; 2000US-019928P

21-MAR-2000; 2000US-019928P

21-MAR-2000; 2000US-019928P

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21-MAR-2000; 2000US-0193053P

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11-APR-2000; 2000US-0194647P

11-APR-2000; 2000US-0195975P

11-APR-2000; 2000US-0195000P
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DB; AAS46079.
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J, Smith V,
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2000US-0198121P.
2000US-01991550P.
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2000US-0199554P.
2000US-019954P.
2000US-019654P.
2000WO-US013705.
2000WO-US014042.
2000WO-US014941.
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2000WS-US033268.
2000WS-US033288.
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V, Watanabe
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atanabe CK,
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, Wood WI, Zhang
                                                                                                                                                                                                                                  Godowski PJ,
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                                                                                                                                                                                                                                  Gurney
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Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumors, such as prostate and breast tumors, in mammals screen for modulators of the compounds. and ő

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Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.

The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of a mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly adrenal, lung, colon, treast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders the animal

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                                 ELLEPKGTGESKGAGESKGVGELRESNSGAENTTETQTSTSTSSLRSDPKLWLALGTVAT
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                                                                                                                                            SSVTSSGVSTATISGSSVTSN-GVSIV-TNSEFHTTSSGISTATNSEFSTASSGISIATN
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RESULT 12
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15-SEP-1999;
07-DEC-1999;
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Grimaldi (
                  Eighty four nucleic acids encoding PRO polypeptides, useful in molecular biology, including use as hybridization probes, and in chromosome and
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2000WO-US004341.
2000WO-US004341.
2000WO-US004414.
2000WO-US005601.
2000US-0187202P.
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99US-0169495P.
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XX ABG95
XC ABG95
XX ABG95
XX Human
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XX Human
XX Antia

10-DEC-2002 ABG95900; ABG95900

(first entry)

standard; protein;

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Human

secreted/transmembrane

protein PRO1342

Human; secreted protein; transmembrane protein; antirheumatic; antiarthritic; osteopathic; sports-related joint problem; articular cartilage defect; osteoarthritis; rheumatoid arthrit

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 596 AA;
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                                                                                              LHDSQVPTSNSNTSVQNMGNTDSVVYSTIQHPPRDTTDNGARLLGNPSAGIQSTYARLAL
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 AGSGTAALTGMHTTSHSA-STAVSEAKPG
                                SGGLRHDMGGLTGGSNSAVNTSNNPPAPG
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19.2%;
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Pred. No. 0.00053;
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Homo sapiens

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17-SEP-1998
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17-SEP-1998
22-SEP-1998
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24-SEP-1998
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2000WO-US004341.

2000WO-US004414.

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98US-0090696P

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23 AUG-2000;
24 AUG-2000;
10-NOV-2000;
01-DEC-2000;
20-DEC-2000;
20-DEC-2001;
01-MAR-2001;
01-MAY-2001;
01-UN-2001;
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2000WO-US032378.
2000WO-US034956.
2001WO-US006520.
2001WO-US006666.
2001WO-US01743.
2001WO-US017800.
2001WO-US017800.
2001WO-US021066.
2001WO-US021059.
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2000WO-US023328
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Eaton DL, Fi Grimaldi JC, Filvaroff C, Gurney Į, Gerritsen Watanabe £, ₩ Goddard A, Wood WI; Godowski

New isolated secreted and transmembrane PRO polypeptide useful for modulating biological activity of a cell, or for treating sports-related joint problems, osteoarthritis or rheumatoid arthritis.

Claim 20; Fig 100; 399pp; English.

CC antibodies which specifically bind to the proteins. The proteins are considered of containing an polypeptide designated as A, B, C or D in a sample consisted of containing an A, B, C or D polypeptide, by contacting the consumpte with a polypeptide designated as E, F, G, H or I (or vice versa) cand determining the formation of a A/E, B/F, B/G, C/H or D/I polypeptide conjugate in the sample, where the formation of the conjugate is conjugate in the sample, where the formation of the conjugate is conjugate in the sample, where A is a PRO10272 polypeptide, B is a PRO20110 polypeptide, C is a conformation of the conjugate is a PRO1096 polypeptide, D is a PRO19760 polypeptide, E is a PRO50010 polypeptide, F is a PRO1096 polypeptide, B is a PRO20110 polypeptide, H is a conformation of a propertide and I is a PRO1890 polypeptide, E is a PRO2033 polypeptide and I is a PRO1890 polypeptide. The sample comprises considered the proteins are useful for linking a bioactive molecule coule to a cell support. The proteins are useful for linking a bioactive molecule causes death of the cell. A, B, C or D or E, F, G, H, or I. The bioactive molecule causes death of the cell. A, B, C, D, E, F, G, H, C, F, G, H, or I can be cell expressing a polypeptide designated as A, B, C, D, E, F, G, H, C, F, G, H, problems, articular cartilage derects, observations are useful as arthritis. Nucleic acids encoding the proteins are useful as hybridisation probes, in chromosome and gene mapping, in the generation of anti-sense RNA and DNA, for the preparation of the proteins, to generate transgenic or knockout animals which are useful in the development and screening of therapeutic useful reagents, for chromosome identification, and in gene therapy. The antibody is useful as a therapeutic agent, in a diagnostic assay and for affinity purification of the protein from recombinant cell culture natural sources. The present proteins, as molecular weight markers for protein electrophoresis purposes, and as therapeutic agents for treating sports-related joint purposems, articular cartilage defects, osteoarthritis or rheumatoid problems, articular cartilage defects, osteoarthritis or rheumatoid The invention relates to an isolated secreted and transmembrane PRO polypeptide having 80 % sequence identity to a sequence appearing as ABG95851-ABG95934 or their associated signal peptide, or a sequence of an extracellular domain of the proteins with their associated signal peptide extracellular domain of the proteins with their associated signal peptide. Also included are the nucleic collaboration of the sequence of a collaboration of the proteins with their associated signal peptide. Also included are the nucleic collaboration of the sequence of a extracellular domain of the proteins with their associated signal peptide. Also included are the nucleic collaboration of the sequence of a collaboration of acids encoding the proteins, vectors, host cells, fusion proteins and

Sequence A

Query Match Best Local Similarity 6.3%; 19.2%; Score 180; DB 5; Pred. No. 0.00053; Length 596

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RESULT 14
ABU58554
ID ABU58
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24-OCT-1997
24-OCT-1997
28-OCT-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human PRO polypeptide #155
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                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                    dog; cat; cow; hors
antibody-dependent
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11-DEC-1997;
17-DEC-1997;
18-DEC-1997;
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                               NSDSSTTSSEASTATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTS----
                                              LHDSQVPTSNSNTSVQNMGNTDSVVYSTIQHPPRDTTDNGARLLGNPSAGIQSTYARLAL
                                                              SGASTATNSDSSTVSSGA---
                                                                                                                                               LG-----NAIPSGVLKDDVVANIEEQAKAAGEEAKQQAIENNAQAQKKYDEQQAKR
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Sequence 5, Appli	Sequence 5, Appli	Sequence 872, App	Sequence 9, Appli	Sequence 330, App	Sequence 16, Appl	Sequence 49, Appl	Sequence 10491, A	Sequence 17307, A	Sequence 22338, A	Sequence 15936, A	Sequence 179, App	•	Sequence 179, App	Sequence 195, App	Sequence 195, App	Sequence 195, App	Sequence 173, App	Sequence 4, Appli

ALIGNMENTS

밁 S 밁 Ś 밁 ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-012-231A-243 S US-10-012-231A-243 Prior Application removed -NUMBER OF SEQ ID NOS: 477 SEQ ID NO 243 LENGTH: 596 Query Match 6.3%; Score 180; DB 2; Best Local Similarity 19.2%; Pred. No. 1.2e-05; Matches 109; Conservative 90; Mismatches 272 APPLICANT: Baker, K Sequence 243, Application US/10012231A Patent No. 6924355 APPLICANT:
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APPLICANT: APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2830P1C23
CURRENT APPLICATION NUMBER: US/10/012,231A
CURRENT FILING DATE: 2002-06-10 181 123 64 50 u ELLEPKGTGESKGAGESKGVGELRESNSGAENTTETQTSTSSLRSDPKLWLALGTVAT 240 SESSTTSSGASTATNSE----SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRAS QRNGVETS--VVLSDQEYARLQSIDPEGKDKFVFTGGRGGAGHAMVTVASDITEARQRIL 180 SDVPGLPVNPMRLAASEITLNDGFEVLHDHGPLDTLNRQIGSSV-FRVETQEDGKHIAVG GNLGHNENVNNSIPPAPPLPSQTDGAGGRGQLINSTGPLGSRALFTPVRNSMADSGDNRA 63 SSVTSSGVSTATISGSSVTSN-GVSIV-TNSEFHTTSSGISTATNSEFSTASSGISIATN GLLLHLEAATNS-----NETSTSANTGSSVISSG------ASTATNSG Fong, Sherman Gao, Wei-Qiang Goddard, Audrey Gurney, Austin L. Hillan, Kenneth J. Godowski, Paul J. Grimaldi, Christopher Ferrara, Napoleone Eaton, Dan 1. Pan, James Botstein, David Kevin P See File Wrapper or Palm 272; Indels Length 596; 98; Gaps 122 49 107

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                                                                                                                                                                                                                                                                                                      Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 243
LENCTH: 596
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 243, Application US/10015389A Patent No. 6936436
                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                        Matches 109;
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/015,389A CURRENT FILING DATE: 2002-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2830P1C48
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Local Similarity 19.2%; Pred. No. 1.2e-05;
nes 109; Conservative 90; Mismatches 272; Indels
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123 QRNGVETS--VVLSDQEYARLQSIDPEGKDKFVFTGGRGGAGHAMVTVASDITEARQRIL 180
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                                          SSVTSSGVSTATISGSSVTSN-GVSIV-TNSEFHTTSSGISTATNSEFSTASSGISIATN
                                                                                SDVPGLPVNPMRLAASEITLNDGFEVLHDHGPLDTLNRQIGSSV-FRVETQEDGKHIAVG
                                                                                                                          GLLLHLEAATNS-----ASTATNSG
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Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth J.
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Desnoyers, Luc
Eaton, Dan 1.
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SEQ ID NO 243
LENGTH: 596
TYPE: PRT
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Patent No. 6936697
                                                                                                                   Query Match 6.3%; Score 180; DB 2; Length 596; Best Local Similarity 19.2%; Pred. No. 1.2e-05; Matches 109; Conservative 90; Mismatches 272; Indels
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APPLICANT:
APPLICANT:
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APPLICANT: Paoni, Nincolas F.
APPLICANT: Paoni, Nicolas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C10
CURRENT ENLIGHTON NUMBER: US/10/006,768A
CURRENT FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 477
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    64 SDVPGLPVNPMRLAASEITLNDGFEVLHDHGPLDTLNRQIGSSV-FRVETQEDGKHIAVG
                                                                                4 GNLGHNPNVNNSIPPAPPLPSQTDGAGGRGQLINSTGPLGSRALFTPVRNSMADSGDNRA 63
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Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J
                                            GLLLHLEAATNS-----NETSTSANTGSSVISSG------
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Hillan, Kenneth J.
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Fong, Sherman
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RESULT 4
US-10-015-671A-243
                                                                                                                                      ; TYPE: PRT ; ORGANISM: Homo sapiens US-10-015-671A-243
                                                                                                                                                                                                 Prior application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 477
SEQ ID NO 243
LENGTH: 596
                                               Query Match 6.3%;
Best Local Similarity 19.2%;
Matches 109; Conservative 9
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APPLICANT:
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/10/015,671A
CURRENT FILING DATE: 2001-12-11
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
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    4 GNLGHNPNVNNSIPPAPPLPSQTDGAGGRGQLINSTGPLGSRALFTPVRNSMADSGDNRA
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Gao, Wei-Qiang
Goddard, Audrey
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Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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                                               90; Mismatches 272;
                                                                  Score 180; DB 2; Length 596; Pred. No. 1.2e-05;
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                                               19;
                                                                                                        APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Pol:
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2839D1C46
CURRENT APPLICATION NUMBER: US/10/015,393A
CURRENT FILING DATE: 2002-06-10
Prior Application removed - See File Wrapper or Pairougher OF SEQ ID NOS: 477
SEQ ID NO 243
LENGTH: 596
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    Query Match
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                                                               TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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Eaton, Dan 1.
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    6.3%;
    Score 180;
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Length 596;
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2830F1C2 CURRENT APPLICATION NUMBER: US/10/011,833A CURRENT FILING DATE: 2002-06-25

Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 477
SEQ ID NO 243
LENGTH: 596
TYPE: DEFM
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US-10-011-833A-243
; Sequence 243, Application US/10011833A
; Patent No. 6951920
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Gao, Wei-Qiang
                                                                                                                                                                                                             Godowski, Paul J.
Grimaldi, Christopher
Gurney, Austin L.
Hillan, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                          Botstein, David
Desnoyers, Luc
Eaton, Dan l.
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90; Mismatches 272;
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US-10-006-041A-243
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                                                                                                                                                                                                                                                                                                                                                                         Sequence 243, Application Patent No. 6951921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 109; Conserv
                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
APPLICANT:
              APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C8
CURRENT APPLICATION UNMERS: US/10/006,041A
CURRENT FILING DATE: 2001-12-06
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Prior Application removed -
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                                                                                                                                      Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Gurney, Austin L.
Hillan, Kenneth J.
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                                                                                                                                                                                                                                                                                                                                           Baker,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGGLRHDMGGLTGGSNSAVNTSNNPPAPG
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Desnoyers, Luc
Eaton, Dan 1.
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                                                                                                                                                                                                                                                                     Ferrara, Napoleone
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                                                                                                                                                                                                                                                                                                                                           Kevin P
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See File Wrapper or
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                                                                                       Polypeptides
 Palm
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RESULT 8
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; ORGANISM: Homo
US-10-006-041A-243
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SEQ ID NO 243
LENGTH: 596
                                                                                                                                                                                                                                                                                                                                                 Sequence 243, Application US/10012064A Patent No. 6953841 GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
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                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                     APPLICANT: Baker, Kevin P. APPLICANT: Botstein, David
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INVENTION: Secreted and Transmembrane Polypeptides INVENTION: Acids Encoding the Same
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                                                                                                                     Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Goddwski, Paul J.
Grimaldi, Christopher J
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                                              Paoni, Nicholas F.
                                                                                    Gurney, Austin L.
Hillan, Kenneth J.
                                                                    Pan, James
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                                                                                                                                                                                                                                                             Desnoyers, Luc
Eaton, Dan 1.
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Pred. No. 1.2e-05;
00; Mismatches 272;
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CURRENT EILING DATE: 2002-07-15
PRIOR APPLICATION NUMBER: 60/098716
PRIOR APPLICATION NUMBER: 60/098723
PRIOR APPLICATION NUMBER: 60/098723
PRIOR APPLICATION NUMBER: 60/098749
PRIOR APPLICATION NUMBER: 60/098750
PRIOR APPLICATION NUMBER: 60/098750
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098821
PRIOR APPLICATION NUMBER: 60/098843
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098843
PRIOR APPLICATION NUMBER: 60/099596
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Best Local S
Matches 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1998-09-09
Prior Application data removed -
NUMBER OF SEQ ID NOS: 477
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6.3%; Score 180; DB 2;
Local Similarity 19.2%; Pred. No. 1.2e-05;
hes 109; Conservative 90; Mismatches 272;
  525 SGGLRHDMGGLTGGSNSAVNTSNNPPAPG
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                                                                  NSDSSTTSSEASTATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTS---
                                                                                                          LHDSQVPTSNSNTSVQNMGNTDSVVYSTIQHPPRDTTDNGARLLGNPSAGIQSTYARLAL
                                                                                                                                                       SESSTTSSGANTAT-NSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTAT
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164 TATNSESSTLSSGASTATN-SDSSTTSSGASTATNSESSTTSSG------ASTAT

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; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 243
; LENGTH: 596
; TYPE: PRT
; ORGANIAM: Homo sapiens
US-10-015-392A-243
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APPLICATION NUMBER: 60/098749
FILING DATE: 1998-09-01
APPLICATION NUMBER: 60/098750
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APPLICATION NUMBER: 60/098723
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                                                         108
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                   181 ELLEPKGTGESKGAGESKGVGELRESNSGAENTTETQTSTSTSSLRSDPKLWLALGTVAT
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o. 6972186
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                                                                                          QRNGVETS---VVLSDQEYARLQSIDPEGKDKFVFTGGRGGAGHAMVTVASDITEARQRIL 180
                                                       SESSTTSSGASTATNSE----SSTPSSGASTVTNSGSSVTSSGASTATNSESSTVSSRAS 163
                                                                                                                                 SSVTSSGVSTATISGSSVTSN-GVSIV-TNSEFHTTSSGISTATNSEFSTASSGISIATN
                                                                                                                                                                    SDVPGLPVNPMRLAASEITLNDGFEVLHDHGPLDTLNRQIGSSV-FRVETQEDGKHIAVG 122
                                                                                                                                                                                                        GLLLHLEAATNS-----NETSTSANTGSSVISSG-----ASTATNSG 49
                                                                                                                                                                                                                                         GNLGHNPNVNNSIPPAPPLPSQTDGAGGRGQLINSTGPLGSRALFTPVRNSMADSGDNRA
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Godowski, Paul J.
Grimaldi, Christopher
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Cao, Wei-Qiang
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Eaton, Dan 1.
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                                                                                                                                                                                                                                                                                               6.3%; Score 180; DB 2; 19.2%; Pred. No. 1.2e-05;
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US-10-011-795B-243
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PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
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PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098821
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CURRENT APPLICATION NUMBER: US/10/011,795B
CURRENT FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
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                                    PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
                                                                           PRIOR FILING DATE: 1998-09-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
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                                                                                        APPLICATION NUMBER: 60/099536
FILING DATE: 1998-09-09
APPLICATION NUMBER: 60/099596
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                                                                                                                                                    FILING DATE: 1998-09-02
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Gao, Wei-Qiang
Goddard, Audrey
Goddowski, Paul J.
Grimaldi, Christopher J.
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Hillan, Kenneth J.
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Eaton, Dan 1.
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ID NOS: 477
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RESULT 11
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                                                                                                                                           APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Besnoyers, Luc
APPLICANT: Eaton, Dan 1.
APPLICANT: Eaton, Dan 1.
APPLICANT: Forg, Sherman
APPLICANT: Fong, Sherman
APPLICANT: Good, Wei-Qiang
APPLICANT: Goodwski, Paul 2
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                                                                                                                                                                                                                                                                                                                            Sequence 243, Application US/10015386A Patent No. 7022498
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LENGTH: 596
TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT:
APPLICANT:
APPLICANT:
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Best Local (
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2830P1C55
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Gao, Wei-Qiang
Goddard, Audrey
                                                                                        Gurney, Austin L.
Hillan, Kenneth J.
                                                                                                                          Godowski, Paul J.
Grimaldi, Christopher
                                                  Pan, James
Paoni, Nicholas F.
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US-10-015-386A-243
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Best Local Similarity
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19.2%; Pred. No. 1.2e-05;
rative 90; Mismatches 272;
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RESULT 12
US-10-012-121A-243
                                                                                                                                                                                             Patent No. 7022817
GENERAL INFORMATION:
                                                                                                                                                                                                               Sequence 243, Application US/10012121A Patent No. 7022817
                                                                                       APPLICANT:
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APPLICANT:
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                                        Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Goddwski, Paul J.
Grimaldi, Christopher J
               Gurney, Austin L.
Hillan, Kenneth J.
                                                                                                                                  Desnoyers, Luc
Eaton, Dan 1.
Pan, James
                                                                                                                       Ferrara, Napoleone
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; ORGANISM: Homo
US-10-012-121A-243
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LENGTH: 596
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                                                                                                                                                               Sequence 243, Application US/10006485A Patent No. 7026448
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C20
CURRENT APPLICATION NUMBER: US/10/012,121A
CURRENT FILING DATE: 2001-12-07
                                                 APPLICANT:
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APPLICANT: Botstein, David
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CURRENT FILING DATE: 2001-12-06
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APPLICATION NUMBER: 60/099815
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FILING DATE: 1998-09-15
APPLICATION NUMBER: 60/100390
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Hillan, Kenneth J.
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OR FILING DATE: 1998-10-22
OR APPLICATION NUMBER: 60/105693
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OR FILING DATE: 1998-10-07
OR APPLICATION NUMBER: 60/103396
OR FILING DATE: 1998-10-07
OR APPLICATION NUMBER: 60/103401
OR FILING DATE: 1998-10-07
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APPLICATION NUMBER: 60/105881
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APPLICATION NUMBER: 60/105882
FILING DATE: 1998-10-27
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FILING DATE: 1998-10-06
APPLICATION NUMBER: 60/103633
FILING DATE: 1998-10-08
APPLICATION NUMBER: 60/103678
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                                                 SGASTATNSDSSTVSSGA---STATNSESSTTSSGAST--
                                                                                LG-----NAIPSGVLKDDVVANIEEQAKAAGEEAKQQAIENNAQAQKKYDEQQAKR
                                                                                                                 N----SESSTVSSRASTATNSESSTT---SSGASTATNSESRTTSNGAGTATNSESSTTS
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Conservative 9
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DR FILING DATE: 1998-09-23
DR APPLICATION NUMBER: 60/101738
DR FILING DATE: 1998-09-24
OR APPLICATION NUMBER: 60/101741
OR FILING DATE: 1998-09-24
OR APPLICATION NUMBER: 60/101743
OR FILING DATE: 1998-09-24
OR FILING DATE: 1998-09-24

APPLICATION NUMBER: 60/101915 FILING DATE: 1998-09-24

APPLICATION

NUMBER:

60/101916

APPLICATION NUMBER: 60/101476 FILING DATE: 1998-09-23 APPLICATION NUMBER: 60/101477

FILING DATE: 1998-09-23 APPLICATION NUMBER: 60/101479

APPLICATION NUMBER: 60/101474
FILING DATE: 1998-09-23
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FILING DATE: 1998-0 APPLICATION NUMBER:

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60/102484 60/102331 FILING DATE: 1998-0 APPLICATION NUMBER:

60/102307

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APPLICATION NUMBER: 60/102240

APPLICATION NUMBER: 60/102207 FILING DATE: 1998-09-24

R FILING DATE: 1998-09-30
R APPLICATION NUMBER: 60/102487
R FILING DATE: 1998-09-30
R APPLICATION NUMBER: 60/102570
R FILING DATE: 1998-09-30
R APPLICATION NUMBER: 60/102571
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FILING DATE: 1998-10 APPLICATION NUMBER:

APPLICATION NUMBER: 60/102687

1998-10-01

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APPLICATION NUMBER: 60/102684

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PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same
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DR APPLICATION NUMBER: 60/099536

DR FILING DATE: 1998-09-09

DR APPLICATION NUMBER: 60/099596

DR FILING DATE: 1998-09-09

DR FILING DATE: 1998-09-09
                                    R APPLICATION NUMBER: 60/099754
RR FILLING DATE: 1998-09-10
RR APPLICATION NUMBER: 60/099763
RR FILLING DATE: 1998-09-10
RR APPLICATION NUMBER: 60/099792
RR FILLING DATE: 1998-09-10
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APPLICATION NUMBER: 60/098821
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/099741
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APPLICATION NUMBER:
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o. 7026449
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Godowski, Paul J.
Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth J.
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Botstein, David
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Eaton, Dan 1.
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RESULT 15
US-10-012-752A-243
Prior application removed
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 243
LENGTH: 596
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Patent No. 70
                                                                                                                                                                                                                                                                                                                                                                GENERAL
                                                                                                                                                        APPLICANT:
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                                                            APPLICANT: Paoni, Nicholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2830P1C24
CURRENT APPLICATION NUMBER: US/10/012,752A
CURRENT FILING DATE: 2002-06-25
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                                                                                                                                                                                               Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J
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                                                                                                                                                                       Gurney, Austin L. Hillan, Kenneth J.
                                                                                                                                                        Pan, James
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Query Match

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                                                                         212 N----SESSTVSSRASTATNSESSTT---SSGASTATNSESSTTSNGAGTATNSESSTTS 264
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                              525 SGGLRHDMGGLTGGSNSAVNTSNNPPAPG 553
                                                                                                                                                                                                                                   303 SESSTTSSGASTATNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATN 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 TATNSESSTLSSGASTATN-SDSSTTSSGASTATNSESSTTSSG------ASTAT 211
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                                                                                                                                                      363 SESSTTSSGANTAT-NSESSTVSSGASTÄTNSESSTTSSGVSTATNSESSTTSSGASTAT 421
                                                                                                                                                                                            411 KPANNTPAQGNVDTPGSEDTMESRRSSMASTSSTFFDTSSIGTVQNPYADVKTS-----
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SSVTSSGVSTATISGSSVTSN-GVSIV-TNSEFHTTSSGISTATNSEFSTASSGISIATN 107
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Search completed: August 1, 2006, 22:14:59 Job time : 53 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
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       2006, 22:25:31 ; Search time 184 Seconds (without alignments)
1404.749 Million cell updates/sec
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                    US-11-134-563-12
US-11-052-554A-20
US-11-057-143-31017
US-11-097-143-27426
US-09-946-374-243
US-10-066-867-100
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US-10-176-913-310
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Sequence 12, Appl Sequence 20, Appl Sequence 310, Appl Sequence 27426, A Sequence 100, App Sequence 100, App Sequence 110, App Sequence 310, App Sequence 100, App Sequence 310, App
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 12, Application US/11134563
Publication No. US20050287569A1
GENERAL INFORMATION:
APPLICANT: Leong, John M.
APPLICANT: Campellone, Kenneth G.
TITLE OF INVENTION: ESPFU NUCLEIC ACIDS AND TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 07917-280001
CURRENT FILING DATE: 2005-05-20
PRIOR APPLICATION NUMBER: US/11/134,563
CURRENT FILING DATE: 2005-05-20
PRIOR APPLICATION NUMBER: US 60/573,600
PRIOR FILING DATE: 2004-05-20
UNMBER OF SEG ID NOS: 26
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 558
TYPE: PRT
ORGANISM: Escherichia coli
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                                     LGNA I PSGVLKDDVVAN I EEQAKAAGEEAKQQA I ENNAQAQKKYDEQQAKRQEELKVSSG
                                                                                                                                     ELLEPKGTGESKGAGESKGVGELRESNSGAENTTETQTSTSTSSLRSDPKLWLALGTVAT
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                                                                                              GLIGLAATGIVQALALTPEPDSPTTTDPDAAASATETATRDQLTKEAFQNPDNQKVNIDE
                     LGNAI PSGVLKDDVVANI EEQAKAAGEEAKQQAI ENNAQAQKKYDEQQAKRQEELKVSSG
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US-10-180-552-310
US-10-180-557-310
US-10-063-502-100
US-10-174-572-310
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US-10-174-579-310
US-10-174-582-310
US-10-175-739-310
US-10-175-740-310
US-10-175-740-310
US-10-176-488-310
US-10-176-985-310
US-10-176-985-310
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; ORGANISM: Escherichia coli 0157:H7
US-11-052-554A-20
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US-11-052-554A-20
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 20
LENGTH: 558
TYPE: POTENTIAL SERVICE SERV
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APPLICANT: Sachdeva, et al.
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE REFERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR APPLICATION NUMBER: US 60/589,227
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-20
PRIOR FILING DATE: 2004-07-206
NUMBER: IN 173/DEL/2004
PRIOR FILING DATE: 2004-07-06
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Best Local Similarity 100.0%; P
Matches 558; Conservative 0;
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NVDTPGSEDTMESRRSSMASTSSTFFDTSSIGTVQNPYADVKTSLHDSQVPTSNSNTSVQ
                                                                                              AGYGLSGAL ILGGGIGVAVTAALHRKNQPVEQTTTTTTTTTTTTSARTVENKPANNTPAQG
                                                                                                                                                                                                        LGNAIPSGVLKDDVVANIEEQAKAAGEEAKQQAIENNAQAQKKYDEQQAKRQEELKVSSG
                                                                                                                                                                                                                                                                                     GLIGLAATGIVQALALTPEPDSPTTTDPDAAASATETATRDQLTKEAFQNPDNQKVNIDE
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                                                        AGYGLSGALILGGGIGVAVTAALHRKNQPVEQTTTTTTTTTTTTSARTVENKPANNTPAQG
                                                                                                                                                                     LGNA I PSGVLKDDVVAN I EEQAKAAGEEAKQQA I ENNAQAQKKYDEQQAKRQEELKVSSG
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Pred. No. 3.6e-177;
); Mismatches 0;
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RESULT 3
US-11-097-143-31017
Secuence 31017, Ap
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US-11-097-143-31017
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PRIOR FILING DATE: 1999-10-19
PRIOR PELICATION NUMBER: 60/161,932
PRIOR APPLICATION NUMBER: 60/164,769
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 1999-12-28
PRIOR PILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
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SOFTWARE: FastSEQ for Windows
SEQ ID NO 31017
LENGTH: 1300
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CURRENT FILING DATE: 2005-04-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                           438 NSTSNSNSNTNDSTGPSETSSTNGLVASGGAG-----GATGAAMLPTP---SQQSTGGK 488
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                                                                                                                                            HAMVTVASDITEARQRILELLEPKGTGESKGAGESKGVGELRESNSGAENTTETQTSTST
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Pred. No. 0.003;
4; Mismatches 2
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                                                                                                  AGAGSEVNGGRSTSLRKSMRVNS
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US-11-097-143-27426
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Best Local :
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 27426
LENGTH: 2586
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Publication No. US20050208558A1
GENERAL INFORMATION:
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ORGANISM: DROSOPHILA
-11-097-143-27426
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PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
PRIOR ADDITORMATOR TOTAL
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                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/191,637 FILING DATE: 2000-03-23
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                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2000-01-12
                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/175,693
131 QGSSSNGDGNSTQ-----SSTTTTTTTTSSDGGEFTTSSDPVVEVSQ--GTNGGNSST
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                                53
                                                                                                                                             h 6.4%; Score 182.5; DB Similarity 19.4%; Pred. No. 0.014;
                             NSMADSGDNRASDVPGLPVNPMRLAASEITLNDGFEVLHDHGPLDTLNRQIGSSVFRVET
                                                              GELLGNPNYVNCVNGKKQLPLLDGSSITDHSASTNTITKIIDDGLSSQTTSSSAPVVDVT
                                                                                              GNLGHNENVNNSIPPAPPLP----SQTDGAGGRGQLIN----STGPLGSRALFTPVR 52
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                                              SAGIQSTYARLALSGGLRHDMGGLTGGSNSAVNTSNNPPAPG
                                                                                            PVSEVAQGSSSIGDGNSTQSSTTTTTTTTTSSDGGQSTTSSDPVVEVSQGTNG---
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PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01 GENERAL INFORMATION: Sequence 243, Appropriate Publication No. APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04 APPLICANT: APPLICANT: APPLICANT: Baker, Kevin P. APPLICANT: Goddard, Audrey Godowski, Paul J. Grimaldi, Christopher J Gurney, Austin L. Hillan, Kenneth J. Tumas, Stewart, Timothy A. Roy, Margaret Ann Smith, Victoria Fong, Sherman Gao, Wei-Qiang Paoni, Pan, James Ferrara, Napoleone Eaton, Dan L. Desnoyers, Luc Botstein, David Application US/09946374 o. US20030073129A1 Nicholas F Daniei 4

DR APPLICATION NUMBER: 60/099596

DR FILING DATE: 1998-09-09

DR APPLICATION NUMBER: 60/099598

DR FILING DATE: 1998-09-09

DR APPLICATION NUMBER: 60/099602

DR FILING DATE: 1998-09-09

DR APPLICATION NUMBER: 60/099642

R APPLICATION NUMBER: 60/05
R FILING DATE: 1998-09-02
R APPLICATION NUMBER: 60/05
R FILING DATE: 1998-09-02
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R FILING DATE: 1998-09-02
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OR FILING DATE: 1998-09-09
OR APPLICATION NUMBER: 60/099741
OR APPLICATION NUMBER: 60/099740
OR APPLICATION NUMBER: 60/099754
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OR APPLICATION NUMBER: 60/099763
OR FILING DATE: 1998-09-10
OR APPLICATION NUMBER: 60/099808
OR FILING DATE: 1998-09-10
OR APPLICATION NUMBER: 60/099815
OR FILING DATE: 1998-09-10
OR APPLICATION NUMBER: 60/099815
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OR APPLICATION NUMBER: 60/100380
OR FILING DATE: 1998-09-15
OR APPLICATION NUMBER: 60/100584
OR FILING DATE: 1998-09-16
OR APPLICATION NUMBER: 60/100667
OR APPLICATION NUMBER: 60/100669
OR APPLICATION NUMBER: 60/100699
OR APPLICATION NUMBER: 60/100919
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                                                                  Sequence 100, Application US/10006867
Publication No. US20020119130A1
GENERAL INFORMATION:
APPLICANT: Eaton, Dan L.
APPLICANT: Filvaroff, Ellen
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DR APPLICATION NUMBER: 60/105000
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DR APPLICATION NUMBER: 60/105002
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DR APPLICATION NUMBER: 60/105104
DR FILING DATE: 1998-10-21
DR APPLICATION NUMBER: 60/105266
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DR APPLICATION NUMBER: 60/105693
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DR FILING DATE: 1998-10-26
DR APPLICATION NUMBER: 60/105694
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Gerritsen, Mary E. Goddard, Audrey Godowski, Paul J.
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CURRENT APPLICATION NUMBER: US/10/006,867
CURRENT FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: 60/063435
PRIOR FILING DATE: 1997-10-29
PRIOR PPLICATION NUMBER: 60/064215
PRIOR APPLICATION NUMBER: 60/082797
PRIOR APPLICATION NUMBER: 60/082797
PRIOR APPLICATION NUMBER: 60/083495
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/085579
PRIOR PILLING DATE: 1998-05-15
PRIOR PILLING DATE: 1998-05-05
PRIOR FILLING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/08759
PRIOR APPLICATION NUMBER: 60/08021
PRIOR FILLING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088021
PRIOR APPLICATION NUMBER: 60/088029
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILLING DATE: 1998-06-04
PRIOR PILLING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088734
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APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
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DR APPLICATION NUMBER: 60/089653

DR FILING DATE: 1998-06-17

DR APPLICATION NUMBER: 60/089952

DR FILING DATE: 1998-06-19

DR APPLICATION NUMBER: 60/090246

DR APPLICATION NUMBER: 60/090444

DR FILING DATE: 1998-06-24

DR APPLICATION NUMBER: 60/090444

DR FILING DATE: 1998-06-24
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OR FILING DATE: 1998-06-10
OR PILING DATE: 1998-06-10
OR PILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/088863
OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/089105
OR FILING DATE: 1998-06-12
OR APPLICATION NUMBER: 60/089514
OR APPLICATION NUMBER: 60/089514
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NR APPLICATION NUMBER: 60/096757
DR FILING DATE: 1998-08-17
DR APPLICATION NUMBER: 60/096949
DR FILING DATE: 1998-08-18
DR APPLICATION NUMBER: 60/096959
APPLICATION NUMBER: 60/097954
FILING DATE: 1998-08-26
APPLICATION NUMBER: 60/097971
FILING DATE: 1998-08-26
APPLICATION NUMBER: 60/097979
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FILING DATE: 1998-06-26
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/096012
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R APPLICATION NUMBER: 60/13
R FILING DATE: 1999-04-27
RA APPLICATION NUMBER: 60/13
REFILING DATE: 1999-06-09
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R FILING DATE: 1998-12-30
R FILING DATE: 1998-12-30
R RPLICATION NUMBER: 60/
R FILING DATE: 1999-01-12
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APPLICATION NUMBER: 09/
FILING DATE: 1999-05-14
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APPLICATION NUMBER: 60/
FILING DATE: 1999-02-09
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FILING DATE: 1999-08-25
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APPLICATION NUMBER: 60/
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FILING DATE: 1999-02-10
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APPLICATION NUMBER: 60/119285
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DR FILING DATE: 1998-10-28

DR APPLICATION NUMBER: 60/106464

DR FILING DATE: 1998-10-30

DR APPLICATION NUMBER: 60/106856

DR FILING DATE: 1998-11-03

DR APPLICATION NUMBER: 60/108807

DR FILING DATE: 1998-11-17

DR APPLICATION NUMBER: 60/112419

DR APPLICATION NUMBER: 60/112412

DR FILING DATE: 1998-12-15

DR APPLICATION NUMBER: 60/112422

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CURRENT FILING DATE: 2002-01-15
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APPLICATION NUMBER: 60/062250
FILING DATE: 1997-10-17
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FILING DATE: 1997-09-18
APPLICATION NUMBER: 60/059266
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APPLICATION NUMBER: 60/063870
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APPLICATION NUMBER: 60/063544
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APPLICATION NUMBER: 60/063541
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APPLICATION NUMBER: 60/066120
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APPLICATION NUMBER: 60/065311
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FILING DATE: 1997-10-31
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APPLICATION NUMBER: 60/063734
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APPLICATION NUMBER: 60/063564
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APPLICATION NUMBER: 60/063486
FILING DATE: 1997-10-21
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APPLICATION NUMBER: 60/066466
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Godowski, Paul J
Gurney, Austin L
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PREPLICATION NUMBER: 60/084639

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DR APPLICATION NUMBER: 60/077632
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DR APPLICATION NUMBER: 60/078886
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DR APPLICATION NUMBER: 60/078939
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APPLICATION NUMBER: 60/083496
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083499
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APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/083495
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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082568
FILING DATE: 1998-04-21
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APPLICATION NUMBER: 60/080333
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APPLICATION NUMBER: 60/081049
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APPLICATION NUMBER: 60/080194
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APPLICATION NUMBER: 60/080327
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FILING DATE: 1997-12-17
APPLICATION NUMBER: 60/068017
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APPLICATION NUMBER: 60/077450
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APPLICATION NUMBER: 60/084414
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FILING DATE: 1998-04-29
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APPLICATION NUMBER: 60/082797
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APPLICATION NUMBER: 60/081195
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APPLICATION NUMBER: 60/069335
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APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088167
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60/089653
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Prior Application removed NUMBER OF SEQ ID NOS: 170 SEQ ID NO 100 LENGTH: 596 TYPE: PRT

ORGANISM: Homo Sapien

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P32308R1C1 CURRENT APPLICATION NUMBER: US/10/063,547 CURRENT FILING DATE: 2002-05-02

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See File Wrapper

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Palm

APPLICANT:

Gurney, Austin L. Watanabe, Colin K. Wood, William I.

APPLICANT

APPLICANT:

APPLICANT:

Grimaldi, Christopher Godowski, Paul J.

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RESULT 8
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Best Local Sim
Matches 109;
                                       GENERAL INFO
                                                                  Sequence 100, A Publication No.
          APPLICANT:
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PRIOR APPLICATION NUMBER: 60/089908
APPLICANT:
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          Filvaroff, Ellen
Gerritsen, Mary
Goddard, Audrey
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; Prior Application removed -
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 100
; LENGTH: 596
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-551-100
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Publication No. US20020183494A1
                                                                                                      TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPE
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3230R1C1
CURRENT APPLICATION NUMBER: US/10/063,551
CURRENT FILING DATE: 2002-05-02
Prior Application removed - See File Wrapper or Palm
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Grimaldi, Christopher J.
Gurney, Austin L.
Watanabe, Colin K.
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GENERAL INFORMATION:
                  Sequence 310, Appropriate Publication No.
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                                       Application US/10174590
                    US20030008352A1
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IS-10-174-590-310

Sequence 310, Application US/10174590

Publication No. US20030008352A1

GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
APPLICANT: Baker, Kevin L.
APPLICANT: Watanabe, Colin K.
APPLICANT: Thure Town and Transmembrane Polypeptides
TITLE OF INVENTION: SERETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P9430R1642
CURRENT FILING DATE: 2002-06-18
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 310
LENGTH: 596
TYPE: PRT
ORGANISM: Homo Sapien
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NUCLEIC

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RESULT 11
US-10-176-758-310
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       Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 310
LENGTH: 596
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                                                                                                                                                                                                                                                                                                                          Sequence 310, Application US/10176758 Publication No. US20030008353A1
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APPLICANT:
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APPLICANT:
APPLICANT:
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                                                                      CURRENT APPLICATION NUMBER: US/10/176,758
CURRENT FILING DATE: 2002-06-21
                                                                                                   FILE REFERENCE: P3430R1C104
                                                                                                                 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
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TYPE: PRT
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Gurney, Austin L.
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19.2%; Pred. No. 0.0031;
tive 90; Mismatches 272
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       APPLICANT: Zhang,Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P343OR1C50
CURRENT APPLICATION NUMBER: US/10/175,737
CURRENT FILING DATE: 2002-06-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 310
                                                                                                                                                                                                                                                                                                             Sequence 310, Application US/10175737 Publication No. US20030013153A1
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Best Local Similarity
Matches 109; Conserv
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LENGTH: 596
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Gurney, Austin L.
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Godowski, Paul
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                                                                                                                                               Watanabe, Colin K. Wood, William I.
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                                                    NSDSSTTSSEASTATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTS---
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US-10-175-737-310
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TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME FILE REFERENCE: P3230RLC1
CURRENT APPLICATION NUMBER: US/10/063,616
CURRENT FILING DATE: 2002-05-03
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 170
SEQ ID NO 100
LENGTH: 596
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                Sequence 100, Application US/10063616 Publication No. US20030013855A1
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Best Local :
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Gurney, Austin L.
Watanabe, Colin K.
Wood, William I.
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Godowski, Paul J.
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                                                                                                      LHDSQVPTSNSNTSVQNMGNTDSVVYSTIQHPPRDTTDNGARLLGNPSAGIQSTYARLAL
                                                                                                                                            SESSTTSSGANTAT-NSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTAT
                                                                                                                                                                                                                    SESSTTSSGASTATNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATN
AGSGTAALTGMHTTSHSA-STAVSEAKPG
                                  SGGLRHDMGGLTGGSNSAVNTSNNPPAPG
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US-10-174-581-310
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Publication No. US20030017540A1
GRMERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Chen, Jian
                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
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APPLICANT:
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C41
CURRENT APPLICATION NUMBER: US/10/174,581
CURRENT FILING DATE: 2002-06-18
RRIOR APPLICATION NUMBER: 10/052586
PRIOR PELICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR PILING DATE: 2002-01-15
PRIOR FILING DATE: 1997-09-18
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Gurney, Austin L.
                                                                                                                                                                                                   Watanabe, Colin K. Wood, William I.
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Godowski, Paul
                                                                                                                                                                                Zhang, Zemin
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DR APPLICATION NUMBER: 60/059266
DR FILING DATE: 1997-09-18
DR APPLICATION NUMBER: 60/062250
DR FILING DATE: 1997-10-17
DR APPLICATION NUMBER: 60/063120
DR FILING DATE: 1997-10-24
DR APPLICATION NUMBER: 60/063121
DR FILING DATE: 1997-10-24
DR APPLICATION NUMBER: 60/063486
DR APPLICATION NUMBER: 60/063486
DR FILING DATE: 1997-10-28
DR APPLICATION NUMBER: 60/063541
DR APPLICATION NUMBER: 60/063541
DR FILING DATE: 1997-10-28
DR APPLICATION NUMBER: 60/063544
DR FILING DATE: 1997-10-28
DR APPLICATION NUMBER: 60/063544
DR FILING DATE: 1997-10-28
DR APPLICATION NUMBER: 60/06354
DR APPLICATION NUMBER: 60/06354
DR APPLICATION NUMBER: 60/06374
DR FILING DATE: 1997-10-31
DR APPLICATION NUMBER: 60/063870
DR APPLICATION NUMBER: 60/063970
DR APPLICATION NUMBER: 60/063971
DR APPLICATION NUMBER: 60/065311

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OR APPLICATION NUMBER: 60/066120
OR FILING DATE: 1997-11-21
OR APPLICATION NUMBER: 60/066466
OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/066466
OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/06935
OR FILING DATE: 1997-12-11
OR APPLICATION NUMBER: 60/069425
OR FILING DATE: 1997-12-12
OR APPLICATION NUMBER: 60/069870
OR FILING DATE: 1997-12-17
OR APPLICATION NUMBER: 60/077450
OR FILING DATE: 1998-03-10
OR APPLICATION NUMBER: 60/077649
OR APPLICATION NUMBER: 60/077649
OR APPLICATION NUMBER: 60/077649
OR FILING DATE: 1998-03-21
OR APPLICATION NUMBER: 60/078886
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079886
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/079866
OR FILING DATE: 1998-03-27
OR APPLICATION NUMBER: 60/080107
OR APPLICATION NUMBER: 60/080104
OR APPLICATION NUMBER: 60/08033
OR FILING DATE: 1998-03-31
OR APPLICATION NUMBER: 60/08033
OR APPLICATION NUMBER: 60/08036
OR APPLICATION NUMBER: 60/08037
OR APPLICATION NUMBER: 60/08039

PRIOR PRIOR PRIOR

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                                     NSDSSTTSSEASTATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTS-----
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US-10-176-483-310
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Matches 109;
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Best Local Similarity
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APPLICANT: Chen, Jian
APPLICANT: Desnoyers, Luc
APPLICANT: Goddard, Audre
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CURRENT APPLICATION NUMBER: US/10/176,483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE TITLE OF INVENTION: ACIDS ENCODING THE SAME
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ORGANISM: Homo
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               NSDSSTTSSEASTATNSESSTVSSGISTVTNSESSTTSSGANTATNSGSSVTS-
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                                                       LHDSQVPTSNSNTSVQNMGNTDSVVYSTIQHPPRDTTDNGARLLGNPSAGIQSTYARLAL
                                                                                                                                         KPANNTPAQGNVDTPGSEDTMESRRSSMASTSSTFFDTSSIGTVQNPYADVKTS-----
                                                                                                                                                                                     SESSTTSSGASTATNSDSSTTSSGAGTATNSESSTVSSGISTVTNSESSTPSSGANTATN
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Wood, William I.
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19.2%; Pred. No. 0.0031;
/ative 90; Mismatches 272; Indels
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Query Match Best Local Sim Matches 109;

Similarity

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Conservative

90;

APPLICATION NUMBER: 60/089598 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089653

PRIOR PRIOR

FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089538 APPLICATION NUMBER: 60/089514

FILING DATE: 1998-06-17

PRIOR PRIOR PRIOR PRIOR PRIOR

APPLICATION NUMBER: 60/089105 FILING DATE: 1998-06-12 APPLICATION NUMBER: 60/089512

FILING DATE: 1998-06-12 FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/089090

FILING DATE: 1998-06-16

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FILLING DATE: 1998-06-11
APPLICATION NUMBER: 60/08863
FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088876

PRIOR PRIOR PRIOR PRIOR PRIOR

FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088861

APPLICATION NUMBER: 60/088826

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APPLICATION NUMBER: 60/088824 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088825 FILING DATE: 1998-06-10

APPLICATION NUMBER: 60/088811 FILING DATE: 1998-06-10

FILING DATE: 1998-06-10 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088740 APPLICATION NUMBER: 60/088738

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1. /BMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

2. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

3. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

4. /BMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

5. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

6. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*

7. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*

8. /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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US-11-376-673-100
US-11-370-673-100
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US-10-471-571A-3948
US-11-251-208-6
US-11-251-208-6
US-11-317-330A-19
US-10-471-571A-2278
US-11-342-171-6
US-11-342-171-6
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US-11-342-171-6
US-11-342-171-6
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US-11-056-355B-87568
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US-10-523-014-8
US-10-530-629-4
US-10-630-629-4
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US-11-056-355B-81599	US-10-449-902-50884	US-11-330-403-9773	US-10-449-902-55274	US-10-953-349-9273	US-10-953-349-9274	US-10-953-349-9275	US-10-449-902-42266	US-10-449-902-41319	US-10-449-902-54423	US-10-471-571A-4496	US-11-256-173-28	US-10-449-902-43102	US-11-333-747A-44	US-10-449-902-41197	US-11-321-421-344	US-11-321-421-341	US-11-283-329-162	US-11-121-154-24	US-11-266-446-94
Sequence 81599,	Sequence 50884,	9773,	Sequence 55274,	Sequence 9273, A	Sequence 9274, I	Sequence 9275, 1	Sequence 42266,	Sequence 41319,	Sequence 54423,	Sequence 4496, Ap	Sequence 28, App	Sequence 43102, A	Sequence 44, Appl	9	•	Sequence 341, App	:-	24,	Sequence 94, Appl
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ALIGNMENTS

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Sequence 310, Application US/10196749

Publication No. US2006094864All

APPLICANT: Baker, Kevin P.

APPLICANT: Baker, Kevin P.

APPLICANT: Bosnoyers, Luc

APPLICANT: Desnoyers, Luc

APPLICANT: Godowski, Paul J.

APPLICANT: Matanabe, Colin K.

APPLICANT: Mond, William I.

APPLICANT APPLICATION NUMBER: 60/062266

PRIOR APPLICATION NUMBER: 60/063120

PRIOR APPLICATION NUMBER: 60/063121

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CURRENT FILING DATE: 2005-04-06
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                                                                                                                                                               APPLICATION NUMBER: 10/063526
FILING DATE: 2002-05-03
APPLICATION NUMBER: 10/006867
                  FILING DATE: 2000-08-24
APPLICATION NUMBER: 09/380137
FILING DATE: 1999-08-25
APPLICATION NUMBER: PCT/US99/12252
FILING DATE: 1999-06-02
APPLICATION NUMBER: 60/087759
                                                                                                                             FILING DATE: 2001-12-06
APPLICATION NUMBER: PCT/US00/23328
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Grimaldi, Christopher
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       1998-06-02
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US-11-376-673-100
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TITLE OF INVENTION: A NUCLEIC ACID UNDEREXPITITLE OF INVENTION: LING TUMOR
FILE REFERENCE: 9330R1C165C
CURRENT APPLICATION NUMBER: US/11/376,673
CURRENT FILING DATE: 2006-03-14
PRIOR APPLICATION NUMBER: 10/063742
PRIOR FILING DATE: 2002-05-09
PRIOR APPLICATION NUMBER: 10/006867
PRIOR APPLICATION NUMBER: 10/006867
PRIOR FILING DATE: 2001-12-06
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Goddard, Audrey
APPLICANT: Gotowski, Paul
APPLICANT: Grimaldi, J. Cl
APPLICANT: Gurney, Austin
                                                                                                                                                                                                                                                                                                            Sequence 100, Application US/11376673 Publication No. US20060160186A1
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Best Local
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Grimaldi, J. Christopher
Gurney, Austin L.
Wood, William I.
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Pred. No. 0.0066;
0; Mismatches 2:
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; PRIOR APPLICATION NUMBER: 60/170262
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 100
; SEQ ID NO 100
; LENGTH: 596
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-376-673-100
                                                                                  Sequence 3535, Application US/11330403

Publication No. US20060159563A1

GENERAL INFORMATION:
APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement FILE REFERENCE: 38-21(5362)B

CURRENT APPLICATION NUMBER: US/11/330,403

CURRENT FILING DATE: 2006-01-12

INUMBER OF SEQ ID NOS: 19250

SEQ ID NO 3535

LENGTH: 1086

TYPE: PRT
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US-11-330-403-3535
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Query Match
Best Local Similarity
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Best Local Similarity
                                                        ORGANISM: Candida albicans SC5314 -11-330-403-3535
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                                                                                                                                                                                                                                                                                                                                                                                   AGSGTAALTGMHTTSHSA-STAVSEAKPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LHDSQVPTSNSNTSVQNMGNTDSVVYSTIQHPPRDTTDNGARLLGNPSAGIQSTYARLAL 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SESSTTSSGANTAT-NSESSTVSSGASTATNSESSTTSSGVSTATNSESSTTSSGASTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATNSESSTLSSGASTATN-SDSSTTSSGASTATNSESSTTSSG-----ASTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QRNGVETS---VVLSDQEYARLQSIDPEGKDKFVFTGGRGGAGHAMVTVASDITEARORIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSVTSSGVSTATISGSSVTSN-GVSIV-TNSEFHTTSSGISTATNSEFSTASSGISIATN 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SDVPGLPVNPMRLAASEITLNDGFEVLHDHGPLDTLNRQIGSSV-FRVETQEDGKHIAVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLLLHLEAATNS-----NETSTSANTGSSVISSG-----ASTATNSG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6.3%; Score 180; DB 7; Length 596; 19.2%; Pred. No. 0.0066; ative 90; Mismatches 272; Indels
6.3%;
19.0%;
Score 180; DB 7;
Pred. No. 0.014;
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                Length 1086;
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APPLICANT: CHIRON SPA
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PRC
FILE REFERENCE: P026927WO
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SegWin99, version 1.03
SEQ ID NO 3948
LENGTH: 2271
TYPE: PRT
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                                                                                                                                US-10-471-571A-3948
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3948, Application US/10471571A Publication No. US20060115490A1 GENERAL INFORMATION:
                                                       Matches 109;
                                                                        Query Match
Best Local
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                                                                                                                                       NAME/KEY: MISC FEATURE
LOCATION: (1)...(2271)
OTHER INFORMATION: hypothetical protein
                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                        ORGANISM: Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               741
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 GKHIAVGQRNGVETSVVLSDQEYARLQSIDPEGKDKFVFTGGRGGAGHAMVTVASDITEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               355 SEQSSSSATSV-----SASETS-----DTSSTQESSSSSEVSSTQE
                     24
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                                                                          Similarity
SQTDGAGGRGQLINSTGPLGSRALFTPVRNSMADS---
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                                                       Conservative 117; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             STAPHYLOCOCCUS AUREUS PROTEINS
                                                                        18.5%;
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                                                                      Score 169; DB
Pred. No. 0.15;
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                                                                                         Length 2271;
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                                                       Indels 144;
                     --GDNRASDVPGLPVN
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US-11-330-403-12380

Sequence 12380, Application US/11330403

Publication No. US20060159563A1

GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Abad, Mark S.
TITLE OF INVENTION: Genes and Uses for Plant Improvement
FILE REFERENCE: 38-21(53629)B
CURRENT APPLICATION NUMBER: US/11/330,403
CURRENT FILING DATE: 2006-01-12
NUMBER OF SEQ ID NOS: 19250
SEQ ID NO 12380
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
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  ESKGAGESKGVGELRESNSG--
                                          -----SFAFNAT--
                                                                                LSDQEYARLQSIDPE----GKDKFVFTGGRGGAGHAMVTVASDITEARQRILELLEPKGTG
                                                                                                                        SIKSDKGAGTASDALET----TVDTL---
                                                                                                                                                              S----EITLNDGFEVLHDHGPLDTLNRQIGSSVFRVETQEDGKHIAVGQRNGVETSVV
                                                                                                                                                                                                      PSTVASVTAGGGHDVVINASDGVLSLGMVSAVGGSVTIDGGTGSILDNNGATANIIANSA
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21.9%; Pred. No. 0.21;
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-AENTTETQTSTSTSSLRSDPKLWLAL
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
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PRIOR FILING DATE: 2004-02-26
PRIOR APPLICATION NUMBER: US 60/450,406
PRIOR FILING DATE: 2003-02-26
NUMBER OF SEQ ID NOS: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Diamandis, Eleftherios P.
TITLE OF INVENTION: Multiple Marker Assay for
FILE REFERENCE: 11757, 0088USWO
CURRENT APPLICATION NUMBER: US/10/544,944
CURRENT FILING DATE: 2005-08-09
LOCATION: (13893).
OTHER INFORMATION:
FEATURE:
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NAME/KEY: misc_feature
LOCATION: (13880)..(13880)
OTHER INFORMATION: Xaa can
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LOCATION: (13877)..(13
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ORGANISM: Homo sapiens
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                                     NAME/KEY: misc_feature
LOCATION: (13893)..(13893)
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LOCATION: (13890)..(13
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14743)..(14747)
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LOCATION: (14737)...(14737)
OTHER INFORMATION: Xaa can
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LOCATION: (14735)..(14735)
OTHER INFORMATION: Xaa can
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LOCATION: (14731)...(14731)
OTHER_INFORMATION: Xaa can
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LOCATION: (14725)..(14727)
OTHER INFORMATION: Xaa can
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14593)..(14594)
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LOCATION: (14581)..(14581)
OTHER_INFORMATION: Xaa can
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LOCATION: (14579)..(14579)
OTHER INFORMATION: Xaa can
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'COATION: (14575)..(14575)
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LOCATION: (14569)..(14571)
OTHER_INFORMATION: Xaa can
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LOCATION: (13940)..(13941)
OTHER INFORMATION: Xaa can
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LOCATION: (13916)..(13916)
OTHER INFORMATION: Xaa can
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                         LOCATION: (14749)..(147
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LOCATION: (13938)...(13938)
OTHER INFORMATION: Xaa can
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LOCATION: (13928)..(139
OTHER_INFORMATION: Xaa
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LOCATION: (14587)..(14
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LOCATION: (13913)..(13914)
OTHER INFORMATION: Xaa can
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FEATURE:

NAME/KEY: misc feature
LOCATION: (16034)...(16034)
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LOCATION:
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LOCATION: (15667)..(15667)
OTHER INFORMATION: Xaa can
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LOCATION: (16021)..(16021)
OTHER INFORMATION: Xaa can
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LOCATION: (16008)...(16008)
OTHER_INFORMATION: Xaa can
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LOCATION: (15996)..(15997)
OTHER INFORMATION: Xaa can
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LOCATION: (15990)..(15994)
OTHER INFORMATION: Xaa can
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LOCATION: (15984)..(15984)
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LOCATION: (15982)..(15982)
OTHER INFORMATION: Xaa can
FEATURE:
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OTHER INFORMATION: Xaa can
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LOCATION: (15978)..(15978)
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LOCATION: (15972)..(15:
OTHER INFORMATION: Xaa
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LOCATION: (15685)..(15686)
OTHER INFORMATION: Xaa can
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LOCATION: (15673)..(15673)
OTHER INFORMATION: Xaa can
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LOCATION: (15671)...(15671)
OTHER INFORMATION: Xaa can
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OTHER INFORMATION: Xaa can
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LOCATION: (15679)..(15683)
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(16025)..(16025)
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(16037)..(16037)
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(16015)..(16015)
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            Sequence 6, Application US/11251208
Publication No. US20060137043A1
GENERAL INFORMATION:
APPLICANT: Puzio, Piotr
APPLICANT: Chardonnens, Agnes
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 APPLICANT:
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LOCATION: (16040)..(160
OTHER_INFORMATION: Xaa
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LOCATION: (16051)..(16
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Shirley, Amber
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Best Local
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PRIOR FILING DATE: 2003-04-15
PRIOR APPLICATION NUMBER: EP 03009728.1
PRIOR FILING DATE: 2003-05-02
PRIOR APPLICATION NUMBER: EP 03016672.2
PRIOR PILING DATE: 2003-08-01
PRIOR PILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: EP 03022225.1
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CURRENT APPLICATION NUMBER: US/11/251,208
CURRENT FILING DATE: 2005-10-14
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APPLICANT: Sarria-Millan, Rodrigo
APPLICANT: McKersie, Bryan
APPLICANT: McKersie, Bryan
APPLICANT: Chen, Ruoying
TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING PROTEINS ASSOCIATED WITH ABIOTIC
TITLE OF INVENTION: STRESS RESPONSE AND PLANT CELLS AND PLANTS WITH INCREASED
TITLE OF INVENTION: TOLERANCE TO ENVIRONMENTAL STRESS
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NUMBER OF SEQ ID NOS: 852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
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                                                                  ARLLGNPSAGIOSTYARLALSGGLRHDMGGLTGGSNSAVN
                                                                                                                                                                                                                                                             EQQAKRQEELKVSSGAGYGLSGALILG--GGIGVAVTAALHRKNQ----PVEQTTTTTT- 398
                                                                                                                                                                                                                                                                                                   TSQVSYSQSTTALQT-----SSFASSSTTEGSETSSQGFSTSSVLVQMPSSISSEFS
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                                                                                                                                 FFDTSSIGTVQNPYADVKTSLHDSQVPTSNSNTSVQNMGNTDSVVYSTIQHPPRDTTDNG
                                                                                                                                                                  SQVSDTPVSYTTSSSSVSQVSDTPVSYTTSSSSVSQVSDTPVSYTTSSSSVSQVSDTSVP
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Pred. No. 0.78;
4; Mismatches
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NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 19
LENGTH: 785
TYPE: PRT
ORGANISM: Homo sapiens
US-11-317-330A-19
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Best Local Similarity 20.6
Matches 127; Conservative
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APPLICANT: SINN, PATRICK L.
APPLICANT: VOYTAS, DAN
APPLICANT: UNIT DAN
APPLICANT: DAI, JUNBIAO
TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO MODIFIED RETROVIRAL
TITLE OF INVENTION: VECTORS FOR RESTRICTED, SITE SPECIFIC INTEGRATION
FILE REFERENCE: IOWA:074US
CURRENT APPLICATION NUMBER: US/11/317,330A
CURRENT FILING DATE: 2005-12-22
PRIOR APPLICATION UNMBER: 60/638,590
PRIOR FILING DATE: 2004-12-22
NUMBER: 60/638,590
PRIOR FILING DATE: 2004-12-22
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                                                                                                                                                     PIASAASIPAGTV----TVNAAQLSSMP--GLQTINLSALGTSGIQVHPIQGL----
                                                                                                                                                                                                 NMGNTDSVVYSTIQHPPRDTTDNGARLLGNPSAGIQS-TYARLALSGGLRHDMGGLTGGS 539
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20.6%; Pred. No. 0.5;
ative 88; Mismatches 260;
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Publication No. US20060115490A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PRC
FILE REFERENCE: P026927WO
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR FILING DATE: 2001-03-27
NUMBER OF SEQ ID NOS: 5642
SOFTWARE: SeqWin99, version 1.03
SEQ ID NO 2278
LENGTH: 2478
TYPE: PRT
ORGANISM: Staphylococcus aureus
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NAME/KEY: MISC_FEATURE
LOCATION: (1)...(2478)
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5.2%; Score 149; DB 6; 1
Local Similarity 18.5%; Pred. No. 2.2;
hes 128; Conservative 101; Mismatches 265;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --SEYKK----DALAKIEDAYNAKVNEADNSNASTSSEIAEAKQKLAELKQTADQNVNQA 1735
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                                                 NDTWNGIDNNDATANSNANATPENT------GOPNVSETTANGKADASPTTPNNSDAA 2122
                                                                                                                                                                                            --SSMASTSSTFFDTSSIGTVQNPYADV--KTSLH------DSQVPTSNSNT 477
                                                                                                                                                                                                                                                                                                                                                 IQIDSTEKQKAIEELETALDQ-------IEAGVNVNADATTEEKEAFTNA 195
                                                                                                                                                                                                                                                                                                                                                                                                                                            TKESIDQSDQLTAE---EKTEALAMÍKQITDQAKQĞITDATTTAEV-EKAKAQĞLEAFDN 1908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SATETATRDQLTKEAFQNPDNQKVNIDELGNAIPSGVLKDDVVANIEEQAKAAGEEAKQQ 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----PKGTGESKGAGESKGVGELRESNSGAENTTETQTSTST 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TPNASQQEINDAKQEVDTELNQAKTNVDQSSTNEYVDNAVKEGK----AKINAVKTF---
     TG--
                                                                                            SVQNMG--NTDSVVYSTIQHPPRDTTDNGARLLGNPSAGIQSTYARLALSGGLRHDMGGL 535
                                                                                                                                                                                                                                                                                              -QPVEQTTTTTTTTTTSAR--TVENKPANNTPAQGNVDTPGSEDTMESRR------
                                                                                                                                                                                                                                                                                                                                                                                                AIENNAQAQKKYDEQQAKRQEELKVSSGAGYGLSGALILGGGIGVAVTAALHRKN-----
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                                                                                                                                                                                                                                               LEDILSKATEDISDQTTNAEIATVKNSALEQLKAQ-RINPEVKKNALEAIREVVNKQIEI 2010
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-GSNSAVNTSNNPP 550
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US-11-342-171-6
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Publication No. US20060111558A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                   Matches 121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 985 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/126
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 3911
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.25
CURRENT APPLICATION DATA:
APPLICATION UNWBER: US/11/342,171
FILING DATE: 27-JAN-2006
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: RECOMBINANT INFECTIOUSLARYNGOTRACHEITIS VIRUS
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 72
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APPLICANT:
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 06-JUI CLASSIFICATION:
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CLASSIFICATION:
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                                                                                                                                                                                           297 HRIDMSGTE---PPGTETTFDCQKMIETPYRALGSNVPRDDSIRPGATLPPFDTAAPDFD 353
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 LGTVATGLIGLAATGIVQALAL---TPEPDSPTTTDPDAA---
                                   TPGESENTLFPTTAPGISTETPSAAHETTQTQSAETVVFTQSPSTESETARSQSQEPWYF 473
                                                                           GTGESKGA-GESKGVGELRESNSGAENTTETQT-----
                                                                                                               TGTSPTPTTVPEPAITTLIPRSTSDMGFFSTARATGSETLSVPVQETDRTLSTTPLTLPL
                                                                                                                                                                                                                                                                     PVLRNVSDGF-----LVKYTPDIDGRAMINVIANYSPADSGSVLAFTAFREGKLPSAIQL
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1185 Avenue of the Americas
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                               5.2%; Score 147; DB 7; Length 985; 20.6%; Pred. No. 0.92; tive 78; Mismatches 264; Indels 1
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                                                                         -STSTSSLRS-DPKLWLA 234
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   271
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; Publication No. US20060111558A1
; GENERAL INFORMATION:
; APPLICANT: Wild, Martha A.
APPLICANT: Cochran, Mark D.
; TITLE OF INVENTION: AND USES THERE
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 Query Match
                                                                                                                                                       TELEFAX: (212) 391-05
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 01
FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                         MOLECULE TYPE:
                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                             NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 39
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 0
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/0 FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2
                                                                             TOPOLOGY:
                                                                                                                                                                                         TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
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                                                                                                               LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          749 EVKFSNDGEVTATCVSTVKSPYRVETNWKVDLVDVMDEISGNSPAGV
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                                                                                         amino acid
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                                                         protein
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                                                                                                                                                                                           278-0400
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 5.2%;
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   Score 147;
   DB 7;
 Length 985;
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APPLICANT: COSENOTE, Sheena M.
APPLICANT: Sasaki, Ken
APPLICANT: Yang, Yan Ping
APPLICANT: Klein, Michel H
APPLICANT: Klein, Michel H
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN OF MORAXELLA
FILE REFERENCE: 1036-921MIS:jb
CURRENT APPLICATION NUMBER: US/11/013,711
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: US/09/361,619
PRIOR APPLICATION NUMBER: US/09/361,619
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 13
US-11-013-711-9
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                                                    Matches 110;
                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                    LENGTH: 2053
TYPE: PRT
ORGANISM: Moraxella
116 GKHIAVG-----QRNGVETSV-----VLSDQEYARLQSIDPEGKDKFVFTGGRG---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     474 TOTPSTEQAALTOTQIAETEALFTQTPSAEQMTFTQTPGAETEAPAQTPSTIPEIFTQSR
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                                                    Conservative
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                                                                                                                                                                       catarrhalis
                                            5.1%; Score 145.5; DB 7;
19.9%; Pred. No. 2.8;
htive 82; Mismatches 218;
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ative 78; Mismatches 264; Indels
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                                               Indels
                                                                                              Length
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US-11-013-711-11
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                                                                                                                                                                                                                                                                                       ; SEQ ID NO 11
; LENGTH: 2314
; TYPE: PRT
                                                                                                                                      Query Match 5.1%; Score 145; DB 7; Length 2314; Best Local Similarity 20.8%; Pred. No. 3.5; Matches 125; Conservative 89; Mismatches 248; Indels 13
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                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Yang, Yan Ping
APPLICANT: Klein, Michel H.
TITLE OF INVENTION: RECOMBINANT HIGH MOLECULAR WEIGHT MAJOR OUTER MEMBRANE
TITLE OF INVENTION: PROTEIN OF MORAXELLA
FILE REFERENCE: 1038-921MIS:jb
CURRENT APPLICATION NUMBER: US/11/013,711
CURRENT FILING DATE: 2004-12-16
PRIOR APPLICATION NUMBER: US/09/361,619
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Loosmore, She APPLICANT: Sasaki, Ken
                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        489 VYSTIQHPPRDTTDNGARLLGNPSAGIQSTYARLALSGGLRHDMG----GLTGGSNSAVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        670 SNGTSGNNKFSVSNAHDNNSLVTAKDLADYLNKVNETADSALP----SFKVQNGDNSNNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     438 MASTS-----STFFDTSSIGTVQN--PYADVKTSLHDSQVPTSNSNTSVQNMGNTDSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       615 ANTDAV----TIKOLKDAKPTLNAGDGISINSNNGDLVDSSGNITTPTYNISVKTTKLN
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                                                                                            26 TDGAGGRGQLINSTGPLGSRALFTPVRNSM------ADSGDNRASDVPGLPV 71
72 NPMRLAASEITLNDGFEVLHDHGPLDTLNRQIGSSVFRVETQEDGKHIAVGQRNGVETSV 131
                                               TIAIGSNAQAIN----YGALALGADTRVDLDYGIALGYGSQILNNNNNNNNNKAYVP--EG 298
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                                                                                                                                         Indels 138;
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NAME/KEY: peptide
LOCATION: (1)..(804)
OTHER INFORMATION: Ceres Seq. ID no.
US-11-056-355B-87568
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US-11-056-355B-87568
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TITLE OF INVENTION: Polypeptides Encoded Thereby
FILE REFERENCE: 2750-1590FUS2
CURRENT APPLICATION NUMBER: US/11/056,355B
CURRENT FILING DATE: 2005-02-14
PRIOR APPLICATION NUMBER: 60/544,190
PRIOR FILING DATE: 2004-02-13
NUMBER OF SEQ ID NOS: 119966
SEQ ID NO 87568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 87568, Application US/11056355B Publication No. US20060150283A1 GENERAL INFORMATION:
                                                                                                                                                Query Match
Best Local :
                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Brover, Vyacheslav APPLICANT: Alexandrov, Nicko
                                                                                                                                                                                                                                                                    TYPE: prt
ORGANISM: Arabidopsis thaliana
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NGSNIKSSKATGNGLF---
                             AASEITLNDGFEVLHDHGPLDTLNRQIGSSVFRVETQED------
                                                                                              PPAPPLPSQTDGAGGRGQLINSTGPLGSRALFTPVRNSMADSGDNRASDVPGLPVNPMRL 76
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-----NVGFKLLHIHPMITSVPTPMGNAIPISEVRDDVVTAYRQEILWQSEEMLKPYT 100
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                                                                                                                                               5.0%;
                                                                 -VVVALSGSSKSKYVVTWAIEKFATEG
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Pred. No. 1
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---HLVLLLGACPEQGALVYEYMENGSLEDRLFQVNNSPPLPWFERF
                              TYARLALSGGLRHDMGGLT-----GGS--NSAVNTSNNPPAPGSHRF
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                                                             YKCNLHHTTAVVKVLQSAENQLSKQFQQELEILSKIRHP
                                                                                                                       REAERKSARDTKEKEKLEGTLGSPOLOYOHFAWEEIMAATSS-FSEELKIG--MGAYGAV
                                                                                                                                                                                      LEELKLKEYEARELA------EKEKQNFEKARRDAESMRERAEREIAQR
                                                                                                                                                                                                                  QEELKVSSGAGYGLSGALILGGGIGVAVTAALHRKNQPVEQTTTTTTTTTTTTSARTV---
                                                                                                                                                                                                                                                                               EEAKQQAIENNA-----
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                                                                                          -KTSLHDSQVPT---SNSNTSVQNMGNTDSVVYSTIQHPPRDTTDNGARLLGNPSAGIQS
                                                                                                                                                        ---ENKPANNT----PAQGNVDTPGSEDTMESRRSSMASTSSTFFDTSSIGTVQNPYADV
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Search completed: August 1, 2006, 22:29:38
Job time : 35 secs

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      Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.
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translocated intimin receptor Tir [imported] - Escherichia coli (strain O157:H7, substrance); Species: Escherichia coli
C;Species: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: A98199
R;Hayyashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genua; Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A98199
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-558 <HAY>
A;Residues: 1-558 <HAY>
A;Cross-references: UNIPROT:Q9R396; UNIPARC:UPIO000D00CA; GB:BA000007; PIDN:BAB37984.1,
A;Genetics:
A;Gene: EC94561 믕 S 밁 5 밁 8 밁 S 밁 á 밁 Ş В S RESULT A98199 Matches Query Match 100.0%; Score 2840; DB 2; Best Local Similarity 100.0%; Pred. No. 6.7e-150; 361 361 301 181 301 241 241 181 121 121 558; 61 13 1 MPIGNLGHNPNVNNSIPPAPPLPSQTDGAGGRGQLINSTGPLGSRALFTPVRNSMADSGD GLIGLAATGIVQALALTPEPDSPTTTDPDAAASATETATRDQLTKEAFQNPDNQKVNIDE GLIGLAATGIVQALALTPEPDSPTTTDPDAAASATETATRDQLTKEAFQNPDNQKVNIDE VGQRNGVETSVVLSDQEYARLQSIDÞEGKDKFVFTGGRGGAGHAMVTVASDITEARQRIL NRASDVPGLPVNPMRLAASEITLNDGFEVLHDHGPLDTLNRQIGSSVFRVETQEDGKHIA 120 AGYGLSGALILGGGIGVAVTAALHRKNQPVEQTTTTTTTTTTTSARTVENKPANNTPAQG LGNAI PSGVLKDDVVANI EEQAKAAGEEAKQQAI ENNAQAQKKYDEQQAKRQEELKVSSG ELLEPKGTGESKGAGESKGVGELRESNSGAENTTETQTSTSTSSLRSDPKLMLALGTVAT NRASDVPGLPVNPMRLAASEITLNDGFEVLHDHGPLDTLNRQIGSSVFRVETQEDGKHIA AGYGLSGALILGGGIGVAVTAALHRKNOPVEQTTTTTTTTTTTSARTVENKPANNTPAQG LGNAI PSGVLKDDVVANI EEQAKAAGEEAKQQAI ENNAQAQKKYDEQQAKRQEELKVSSG ELLEPKGTGESKGAGESKGVGELRESNSGAENTTETQTSTSTSSLRSDPKLWLALGTVAT VGQRNGVETSVVLSDQEYARLQSIDPEGKDKFVFTGGRGGAGHAMVTVASDITEARQRIL MPIGNLGHNPNVNNSIPPAPPLPSQTDGAGGRGQLINSTGPLGSRALFTPVRNSMADSGD Conservative 0 Mismatches 0 Length Indels 558; o ; Gaps 420 360 360 300 300 240 180 180 120 240 60 60

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probable translocated intimin receptor protein tir [imported] - Escherichia C;Species: Escherichia coli C;Species: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004 C;Accession: E86045 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, S29-533, 2001 A;Title: Genome sequence of enterohemorrhagic Escherichia coli 0157:H7. A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: E86045
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                                      NMGNTDSVVYSTIQHPPRDTTDNGARLLGNPSAGIQSTYARLALSGGLRHDMGGLTGGSN
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A;Status: preliminary; translated
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A; Residues: 1-2232 <GEI>
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les 127; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STNSQTGSTVTMGSSSTSGVSTSSASSTQPQMSTSQGSSAGSTVASSTASPAASSTAPSS
                                                                              VSTSTVPSSTGTMGSTSSGTVGSTISESSTTASASSQTGSTVTMG---SSSTSGVSTSS 1887
                                                                                                                                                                                            DISSIGTV----
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                                                                                                                                                                                                                                                                                                            GSSAGSTVASSTTGLVSTSTVPSSTGTMGSTSSGTVGSTISESSTAASASSQTGSTVTMG
                                                                                                                                                                                                                                                                                                                                                                                    TISESSTTASA----SSQTGSTVTMGSSSTSGV-----STSSASSTQPQMSTSQ
                                                                                                                                                                                                                                                                                                                                                                                                                          TATRDQLTKEAFQNPDNQKVNIDELGNAIPSGVLKDDVVANIEEQAKAAGEEAKQQAIEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QMSTSQGS-----SAGSTVASSTAGLVSTSTV-----PSSTGTMGSTSSGTVGS
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                                                                                                              PPRDTTDNGARLLGNPSAGI-----QSTYARLALSGGLRHDMGGLTGGSNSAVNTSN 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----MVTVASDITEARORILELLEPKGTGESKGAGESKGVGELRESNSGAENTTET 216
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21.2%;
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Pred. No. 0.0056
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1291 <CAT>
                                                                                                                                                                                                                           hypothetical protein 115C2.10 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T13389
R;Salles, C.; Valenti, P.; Darlamitsou, A.; Henderson, N.; Campbell, L.; Glosubmitted to the EMBL Data Library, May 1999
A;Description: Sequencing the distal X chromosome of Drosophila melanogaste:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: T2569;
A;Fatus: preliminary; translated from GB/EMBL/DDBJ
A;Gtatus: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1229 <FUL>
A;Residues: 1-1229 <FUL>
A;Cross-references: UNIPROT:Q94185; UNIPARC:UPI000017B8FF; EMBL:U67956; PIDN:AAB07691.1
A;Cross-references: Gurain Bristol N2; clone F16F9
                                                                                    A; Cross-references:
C; Genetics:
                                                                                                                                                                                         A; Reference number: A; Accession: T13389
                                                                                                                                                                                                             A; Description: Sequencing A; Reference number: Z17665
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R;Fulton, B.
submitted to the EMBL Data Library, August 1996
A;Bescription: The sequence of C. elegans cosmid F16F9
A;Reference number: Z20071
A;Accession: T25697
A; Introns: 238/3; 1: A; Note: EG:115C2.10
                                                            A; Cross-references: FlyBase: FBgn002038:
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Best Local S
Matches 90
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Introns: 35/1; 361/1;
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90; Conserv
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                      1225/1
                                                                                                      UNIPROT:077261; UNIPARC:UPI0000078D1B;
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                                                                                                      EMBL:AL031581; NID:e1320978;
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RESULT 6
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text
C;Accession: A53577
R;Wu, K.; Fregien, N.; Carraway, K.L.
J. Biol. Chem. 269, 11950-11955, 1994
A;Title: Molecular cloning and sequencing of the mucin :
A;Reference number: A53577; MUID:94216302; PMID:8163496
A;Accession: A53577
A;Accession: A53577
A;Status: preliminary
A;Molecule type: mRNA
   밁
                                                                                                                                          C; Keywords: glycoprotein
                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-1630 <WUA>
A;Cross-references: UNIPARC:UPI000017C8BB; GB:U06746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 IENNAQAQKKYDEQQAKRQEELKVSSGAGYGLSGALILGGGIGVAVTAALHRKNQPVEQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 HAMVTVASDITEARQRILELLEPKGTGESKGAGESKGVGELRESNSGAENTTETQTSTST 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        540
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                                 12
 28
                                 VNNSIPPAP----PLPSQTDGAGGRGQLINSTGPLGSRALFTPVRNSMADSGDNRASDVP 67
VNTSTTSAPKTSTALPSSTNPSOMTSOVSNPTA----SSYRMTKNTGQASPMVTSSSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MKRSPILDEVIELG--TSLSNGGAGRG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LRH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENQQQQATRRSCSPTPAYKKNLLASFDPDPPSTQGIKEQLKDESVTYSPVKQKRSRRAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGTVQ-----NPYADVKTSLHDSQVPTSNSNTSVQNMGNTDSVVYSTIQH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTNSSSSSNKATTITNCNNHNSNNSSRINHNSNLSSRLSVKSRKPAPSEASSIPSSTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTTTTTTSARTV---ENKPANNTPAQGNVDTPGSEDTMESRRSSMASTSSTFFDTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAEEPOPEKS-EEKOOEOOKRVTRNSAGRVGL-----VARLATAHNNN----IA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SQQRQLRRSERQKEKLTD-----GESSD---TSSEQQKK----EQKQQDHQLPQKMFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LTKEAFQNPDNQKVNIDELGNAIPSGVLKDDVVANIEEQAKAAGEEAKQQ-----A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSLRSDPKLWLALGTVATGLIGLAATGIVQALALTPEPDSPTTTDPDAAASATETATRDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAGATTVSSVA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --QHHFHHHHHHHHHHHHHOQHASTGAEATAAVQQMAAMQKPG------VGGTGAAG 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGSSVFRVETQEDGKHIAVGQRNGVETSVVLSDQEYARLQSIDPEGKDKFVFTGGRGGAG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EATAAVSLLEKKLPNVVVSPLTMKELRQKGMTKYDAEMIMANAAYQQQHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RAS-----DVPGLPVNPMRLA-----ASEITLNDGFEVLHDHGPLDTLNRQ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSTSNSNSNTNDSTGPSETSSTNGLVASGGAG-----GATGAAMLPTP---SQQSTGGK 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STASADEVI------APVVAASISLPSKAPVVLMPRCKPAQMAIAALHQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NLGHNPNVNNSIPPAPPLPSQTDG---AGGRGQLINSTGPLGSRALFTPVRNSMADSGDN 61
                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DMGGLTGGSNSAVNTSNNPPAPGSHR
                                                                                       6.1%;
20.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPRDTTDNGARL-LGNPSAGIOST-----YARLALSGG
                                                                   70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74;
                                                                                       Score 172.5; D
Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----AGAGSEVNGGRSTSLRKSMRVNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 187; DB 2;
Pred. No. 0.014;
                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                        12-Apr-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -APGSHR
                                                                                                        DB 2;
                                                                     272;
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                                                                       Indels
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                                                                                                          1630
                                                                       203;
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 82
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A;Experimental source: clone C;Genetics:	QY 24 SQTDGAGGKGQLINSTGFLGSKALFTPVENSMADSGDNRASDVPGLPVNPMRLAASETTL 83
A;Residues: 1-487,536-1192 < A;Cross-references: UNIPARC:	Matches 103;
etr	atch 6.1%; Score 172.5; DB 2; Length 2271; cal Similarity 19.5%; Pred. No. 0.19;
A;Accession: T23144 A;Status: translated from GB A;Molecule type: DNA A;Residues: 1-1192 <wil3> A;Cross-references: UNIPARC: A;Experimental source: clone</wil3>	A;Molecule type: DNA A;Residues: 1-2271 <kur> A;Cross-references: UNIPROT:Q99QY4; UNIPARC:UPI00000CABB3; GB:BA000018; PID:g13702612; F A;Experimental source: strain N315 C;Genetics: A;Gene: SA2447</kur>
A; Experimental source: clone A; Experimental source: clone R; McMurray, A. submitted to the EMBL Data L A; Reference number: Z19696	e: Whole genome sequencing of meticillin-res rence number: A89758; MUID:21311952; PMID:11 ssion: P90073 us: preliminary
A;Status: translated from GB A;Molecule type: DNA A;Residues: 1-487,536-1192 < A:Cross-references: UNIPARC:	R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K. Lancet 357, 1225-1240, 2001
A; Restautes: 1-1122 (WILL) A; Cross-references: UNIPROT: A; Experimental source: clone A; Accession: T18610	C;Species: Staphylococcus aureus C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 C;Accession: F90073
A;Accession: T18611 A;Status: translated from GB A;Molecule type: DNA	protein GB2447 [imported] - Graphy]ocoopie autoro (strain
submitted to the EMBL Data L A;Reference number: Z18997	Db 626 TMAVTTQGSTPATTEISVTPS 646
C;Accession: T18611; T18610; R:MCMnrray A	Qy 531 DMGGLTGGSNSAVNTSNNPPA 551
ns: probable serin s: Caenorhabditis	Db 572 SSSDQVQVETTSQTTLSDATTTSHAPRESSSPPSTSDILTTMASTEGTSGDTGH 625
le sı	Qy 472 TSNSNTSVQNMGNTDSVVYSTIQHPPRDTTDNGARLLGNPSAGIQSTYARL-ALSGGLRH 530
RESULT 8	523STVSPLSTSTQETSTQELTSSQSQHTGSMKTTHNPQTTRNTEVTTTLSA
Db 1373 TSTSTSTSLSD	412 PANNTPAQGNVDTPGSEDTMESRRSSMASTSSTFFDTSSIGTVONPYADVKTSLHDSOVP
Qy 500 TTDNGARLLGNPSA : : :	Db 475 APSVSSSSPSPSTEGTSV-DTGLTTAVTTQDSTPATTQGSLTSSSQTL 522
Db 1316 SMSTSDSISTS	417 TILSQSQHTGGMKTTRNPQRTTPTEVTTSTLSASSSDQVQVETTSRATLSPDTTTTSH
441	299 DELGNAIPSGVLKDDVVANIEEQAKAAGEEAKQQAIENNAQAQKKYDEQQAKR
Db 1265 TSISESTSTFKSES	Db 357 PPSTSVILTHGHREGTSGDTGHTMAVTTQGSTPATTEISVTPSTQKMSPVSTFSTSTQEI 416
1207	Qy 274 298
323	297 QSQHTGIMKTTSRTQTTTPTEVTTRTLSASSSDHRQAETSSQTTLSPDTTTTSHAPRESS
Db 1161 LSTSESDSISESTS	OV 247 ATGIVOALALT
263	205ESNSGAENTTETOTSTSTSSLRSDPKLWLALGTVATGLIGLA
Db 1102 SISTSFSDSTSDSK	Db 177 STPATTEISVTPSTQKMSPVSTFSTSTQEITTLSQSQHTGGMKTTRNPQTTGTTEVTTTL 236
1054	Qy 172 ITEA
144	127TTLSPDTTTTSHAPRESSSPPSTSVILTTTASTEGTSGDTGHTMAVTTQG
Db 1012 SDSISTSGSLSASD	117 KHIAVGORNGVETSVVLSDOBYARLOSIDÞEGKDKFVFTGGRGGAGHAMVTVASD
Qy 84 NDGFEVLHDHGPLD :	
Db 974 SLSDSTSTSGSVSG	68 GI.PVNDWBI.BASRITINDRRUH.TVRRDDH.TT.NDCTCSCVRBVRTTDBDC

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                                                                                                                                   TSKSDSISTSTSLSGSTSESESDSTSSSESKSDSTSMSISMSQSTSGS 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TSTS--DSIS-EAISASESTSISLSESNSTSDS------ESQS 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TETATRDQLTKEAFQNPDNQKVNIDELGNAIPSGVLKDDVVANIEEQA 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SKSAŠTASŠESIŠQSASTSTSČSVSTS-TSLSTSNSERTSTSVSDSTŠ 1160
                                                                 SAGIQSTYARLALSGGLRHDMGGLTGGSNSAVNTSNN 548
                                                                                                                                                                                                                                                                          ESVSTSLSMSTSTSL----SNST----SLSTSLSDSTSDSKSDSLST 1315
                                                                                                                                                                                                                                                                                                                                                                                                                    TSESTSESVSSSTSESTSLSDSTSESGSTSTSLSNS--TSGSASISTS 1264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIENNAQAQKKYDEQQAKRQEELKVSSGAGYGLSGALILGGGIGVAVT 380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQSGSTSTSTSTSASVRTS-----ESQSTSGSMSASQS---DSM 1101
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                                                                                                                                                                                                     TVQNPYADVKTSLHDSQVPT-SNSNTSVQNMGNTDSVVYSTIQHPPRD 499
                                                                                                                                                                                                                                                                                                                                            TTTTTTTTTSARTVENKPANNTPAQGNVDTPGSEDTMESRRSSMAS 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POT-STSTSSLRSDPKLWLALGTVATGLIGLAATGIVQALALTPEPDS 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SDSKSMSVSSS---MSTSQSG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTLNRQIGSSVFRVETQEDGKHIAVGQRNGVETSVVLSDQEYARLQS 143
---STSTSLSLSASM--NQSGV--DSNSASQSASN 1411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---STSESLSDSQ----ST 1053
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specific protein kinase (EC 2.7.1.-), long splice form - Caeno s/threonine kinase, short splice form

3B/EMBL/DDBJ

Library, October 1996

T:Q9TW45; UNIPARC:UPI000007ECA3; EMBL:Z81027; PIDN:CAB54179.1;

38/EMBL/DDBJ

<WIL2>
C:UPI000017BD4F; EMBL:Z81027; PIDN:CAB54178.1; GSPDB:GN00023;
ne AH10

Library, June 1997

3B/EMBL/DDBJ

<WIL4>
C:UPI000017BD4F; EMBL:Z96102; PIDN:CAB54262.1; GSPDB:GN00023;
ne H39E23 C:UPI000007ECA3; EMBL:Z96102; PIDN:CAB54263.1; GSPDB:GN00023; ne H39E23 3B/EMBL/DDBJ

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A. A. A. S. S. S.

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hypothetical protein PA1874 [imported] - Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change C;Accession: A83412
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; K port, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: A83412
                                                                                                                                                                                                                                              RESULT 9
A83412
A;Molecule type: DNA
A;Residues: 1-2468 <STO>
A;Cross-references: UNIPROT:Q912M3; UNIPARC:UPI00000C54E3; GB:AE004613; GB:AE004091;
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                                                    A;Status: preliminary
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;Introns: 10/3; 33/3; 67/3; 139/2; 183/3; 451/3; 487/3; 535/3; 631/1; 825/2; 914/3; 992;
;Reywords: alternative splicing; ATP; phosphotransferase; serine/threonine-specific protein kinase, long splice form #;
1-1192/Product: probable serine/threonine-specific protein kinase, short splic
;1-487,536-1192/Product: probable serine/threonine-specific protein kinase,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SRSATTNSANMGASSGGAAAAASATNQLSGAPSSTGASSQQYHPKAPSSSSSSST----
                                                                                                                                                                                                                                                                                                           SMTQPVSGRAGTIGASQGQQTAAALAAIREQSGPIAPGA
                                                                                                                                                                                                                                                                                                                                                                        NROTFHGKTEKDKGGDDSSDEIGETPGNVSIGATGPSANNAEATIWSKLSKLTRRDHNRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VEOTTTTTTTTTTSARTVENKPANNTPAQGNVDTPGSEDTMESRRSSMASTSSTFFDTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KESKPSMIHQSPSMPPSQMMTAMESLKLSESGQTG--GPTVATGGPPQRATS-----QQM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TEPVIREDDDENNSENONGNVPLIGGVGPQTSPAVQVPTEDATSSSDKEQQQQKASSETP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQQQQYMNQLTSSTMMSKLINKTPAAGGTAATSSSSSSSATSTA---PLQKSGSQISHAP
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20.3%;
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Pred. No. 0.15;
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A; Molecule type: DNA
A; Molecule type: DNA
A; Mesidues: 1-796 < WIL>
A; Cross-references: UNIPARC: UPI000017BD37;
A; Cross-references: Clone F27E5
                                                                                                                                                                                                                                                                             hypothetical protein ZK945.10 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te:
A; Map position: 2
A; Introns: 62/3; 124/3; 169/1; 216/1;
                                         C;Genetics:
A;Gene: CESP:ZK945.10
                                                                                                                                                          A; Status: preliminary;
                                                                                                                                                                               submitted to the EMBL Data A; Reference number: Z19425 A; Accession: T21460
                                                                                                                                                                                                                                           R; Wilkinson,
                                                                                                                                                                                                                                                              C; Accession:
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C;Genetics:
A;Gene: PA1874
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 VGQRN-----GVETSVVLSDQEYARLQSIDPEGKDKFVFTGGRGGA---GHAMVTVAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          746 VDSVAPATPVINP----SNGTTLSGTAEP-----GSSV----TLTDGNGNP
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Pred. No. 0.43;
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262/3;

371/1;

581/3;

608/1

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RESULT 11
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
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A; Residues: 1-971 < HAY>
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                              124 --RNGVETSVVLSDQEYARLQSIDPEGKDKFVFTGGRGGAGHAMVTVASDITEARQRILE
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VARN---ASAVAQNTAAAKKSASDAS-----TSAREAATHA--TDAADSARA-----
                                                             SVILLVEGFPPSHAGTITVYEDSOP
                                                                                        SEITLNDGFEVLH-----DHGPLDTLNRQIGSSVFRVETQEDGKHIAVGQ-----
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Pred. No. 0.11;
9; Mismatches 223
                                                                                                                                       Score 164; DB Pred. No. 0.18;
                                                                                                                        Mismatches 198;
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C85693
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A; Residues: 1-973 <STO>
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   AALSASAASTSAGQASASATAA----GKSAESAASSASTATTKAGEATEQASAAASSASA
                                                                                                                                                                                                                  LLEPKGTGESKGAGESKGVGELRESNSGAENTTETQTSTSTSSLRSDPKLWLALGTVATG
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                              AGYGLSGALILGGGIGVAVTAALHRKNQPVEQTTTTTTTTTTTTSARTVENKPANNTPAQ-
                                                                                        GNAIPSGVLKDDVVANIEEQAKAAGEEAK-QQAIENNAQAQKKYDEQQAKRQEELKVSSG
                                                                                                                        SAGAAKTSETNAAVSQQSAATSASTATTKASEAASSARDASASKEAAKSSETSAAS----
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21.2%;
                                                              SASSAASSATAAGNSAKAAKTSETNAKSSETAAEQSASAAAGSK--TA
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MUID:21074935; PMID:11206551
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A;Introns: 42/1; 78/3; 106/3; 135/2; 161/2; 224/1
C;Superfamily: yeast glucan 1,4-alpha-glucosidase homolog; glucan 1,4-alpha-glucosidase
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A;Residues: 1-1275 <GEI>
A;Cross-references: UNIPROT:076602; UNIPARC:UPI0000082AAD; EMBL:AF077538; PIDN:AAC64622.
A;Experimental source: strain Bristol N2; clone H02F09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Geisel, C.; Harmon, G.
submitted to the EMBL Data Library, July 1998
A;Description: The sequence of C. elegans cosmid H02F09.
A;Reference number: Z21330
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   QNMGNTDSVVYSTIQHPPRDTTDNGA 505
                                                          STNTPDSTESTISGSTISGSTGSTESSTMS
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                                                                                          NVDTPGSEDTMESRRSSMASTSSTFFDTSSIGTVQNPYADVKTSLH-DSQVPTSNSNTSV 479
                                                                                                                             VSGSTGSTGESTILESSVSTVSVSTGSTITDGSTASRSSVSTVSASTESTVSGGSSASIG
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                                                        -GSTETSTSGGSTVSGSSLSTS-
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                                                                                                                                              RESULT 15
G89287
                                                protein H39E23.1 [imported] - Caenorhabditis elegans (;Species: Caenorhabditis elegans C;Date: 10-May-2001 #sequence_revision 10-May-2001 #C;Accession: G89287 R;anonymous, The C. elegans Sequencing Consortium.
               R;anonymous, The C. ele
Science 282, 2012-2018,
A;Title: Genome sequence
A;Title: Genome sequence of the nematode C. elegans: a platform A;Reference number: A75000; MUID:99069613; PMID:9851916
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A; ACCESSACO.
A; SCATUS: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Cross-references: UNIPROT: 084419; UNIPARC: UPI0000047BD1;
A; Cross-references: Serotype D, Strain UM-3/Cx
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R;Stephens, R.S.; Kalman, (
Science 282, 754-759, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change
C;Accession: A71517
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Best Local Similarity
Matches 120; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al protein pmpC - Chlamydia trachomatis (serotype D, Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RILELLEPKGTGE-----SKGAGESKGVGELRESNSGAENTTETQTSTSTSSLRSDPK
                                                                                        NTLPNSNIDQSNENTDESSDSHTEEITDESVSSSSESGSSTPQDGGAASSGAPSGDQSIS
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ANACLAKSYAASTDSSPVSNSSGSEEPVTSSSDSDVTASSDNPDSSS
                                           --AGIQSTYARLALSGGLRHDMGG---LTGGSNSAVNTSNNPPAPGS
                                                                                                                                        TSLHDSQVPTSNSNTSVQNMGNTDSV----VYSTIQHPPRDTTDNGARLLGNPS-----
                                                                                                                                                                                                                                      SEDTMESRRSSMASTS--STFFDTSSIGT--VQNPYADV----
                                                                                                                                                                                                                                                                                                                                      VT------AALHRKNQPVEQTTTTTTTTTTTSARTVEN---KPANNTPAQGNVDTPG 426
                                                                                                                                                                                                                                                                                                                                                                                       IYGKKAKLSRINN-------LELSGNSSQDVGGGLCLTESVEFDAIGSL
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22.8%; Pred. No. 0.
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#text_change 10-May-2001

for investigating biolog

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A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_elega;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and A;Accession: G89287
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1246 <STO>
A;Cross-references: UNIPARC:UPI000017A692; GB:chr_V; PIDN:CAB09532.1; PID:g3878100; GSPU
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A;Map position: 5
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                                                                                                                                                                                                           LLCDNGLRLWPSMIHQSP-----SMPPSQMMTAMESLKLSESGQTGGPTVATGGPPQRA
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Total number of hits satisfying chosen parameters:
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Q962D1_DROME
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,	Q4W9Q8 ASPFU	Q59XL0_CANAL	Q6UXCS_HUMAN	Q5SQA0_HUMAN	Q9BMQ0_DROME	Q9V602_DROME	Q7RW61_NEUCR	Q5CTC7_CRYPV	Q7KUH2_DROME	Q8CMU7_STAES	Q9W5E0_DROME	077261_DROME	Q4IHX0_GIBZE	Q4PFY2_USTMA	
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ALIGNMENTS

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RESULT 1
Q9R396_ECOLI
ID Q98396;
AC Q9R396;
DT 01-MAY-2000, E
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DT 07-FEB-2006, E
DT 0
                           EMBL; AF125993; AAD29391.1; -; G

EMBL; AF071034; AAC31506.1; -; G

EMBL; DQ007021; AAX25392.1; -; G

PIR; A98199; A98199.

PIR; E86045; E86045.

HSSP; Q9KWH9; 1F02.
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                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
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STRAIN=CPG7;
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STRAIN=AFCC43895, and EDL933;
MEDLINE=98339885; PubMed=9673266;
Perna N.T., Mayhew G.F., Posfai G., Elliott S.,
Raper J.B., Blattner F.R.;
"Molecular evolution of a pathogenicity island
Escherichia coli 0157:H7.";
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MEDLINE=99242825; PubMed=10225900;
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Commons Attribution-NoDerivs License
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Q7DB77; Q7A9Q1;
JT 05-JUL-2004, integrated into Unit O5-JUL-2004, sequence version 17.
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GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR003536; Tir_rcpt.
Pfam; PF07489; Tir_receptor_M; 1.
Pfam; PF07549; Tir_receptor_M; 1.
Pfam; PF07490; Tir_receptor_N; 1.
PRINTS; PR01370; TRNSINTIMINR.
     NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA] STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;
                                                                                                       Escherichia coli O157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
                                                                                                                                                             Name=tir; OrderedLocusNames=ECs4561, Escherichia coli O157:H7.
                                                                              NCBI_TaxID=83334;
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SEQUENCE
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STRAIN-0157:H7 / Sakai / RIMD 0509952 / EHEC;
MEDLINE-21156231; PubMed=11258796; DOI=10.1093/dnares/8.1.11;
MASIDINE-10.1093/dnares/8.1.11;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga Kuhara S., Shiba T., Hattori M., Shinagawa H.;
Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
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"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.", Nature 409:529-533(2001).
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GO; GO:0004872; F:receptor activity;
GO; GO:0007155; P:cell adhesion; IE;
InterPro; IPR003536; Tir receptor C; 1.
Pfam; PF07489; Tir receptor M; 1.
Pfam; PF07490; Tir receptor N; 1.
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Paton A.W., Manning P.A., Woodrow M.C., Paton J.C.;
"Translocated intimin receptors (Tir) of Shiga-toxigenic Escherichia coli isolates belonging to serogroups O26, O111, and O157 react with sera from patients with hemolytic-uremic syndrome and exhibit marked
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01-NOV-1998, sequence version
07-FEB-2006, entry version 18.
Translocated intimin receptor
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SEQUENCE
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GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR003536; Tir_rcpt.
Pfam; PF07489; Tir_receptor_C; 1.
Pfam; PF03549; Tir_receptor_N; 1.
Pfam; PF07490; Tir_receptor_N; 1.
PRINTS; PR01370; TRNSINTIMINR.
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PubMed=16272509; DOI=10.1128/JCM.43.11.5715-5720.2005;
Pubmed=16272509; DOI=10.1128/JCM.43.11.5715-5720.2005;
Garmendia J., Ren Z., Tennant S., Midolli Viera M.A., Chon Whale A., Azzopardi K., Dahan S., Sircili M.P., Franzolin Trabulsi L.R., Phillips A., Gomes T.A., Xu J., Robins-Brow
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Bacteria; Proteobacteria; Gammaproteobacteria;
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NRASDVPGLPVNPMRLAASEITLNDGFEVLHDHGPLDTLNRQIGSSVFRVETQEDGKHIA
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Q58188 ECOLI
Q58188;
Q58188;
Q58-APR-2005,
26-APR-2005,
27-FEB-2006,
                            InterPro; IPR003536; Tir_rcpt.
Pfam; PF07489; Tir_receptor_C;
Pfam; PF03549; Tir_receptor_N;
Pfam; PF03549; Tir_receptor_N;
PRINTS; PR01370; TENSINTIMINR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.
STRAIN-Baisman's Run stream;
PubMed=15870341; DOI=10.1128/AEM.71.5.2511-2519.2005;
Higgins J.A., Belt K.T., Karns J.S., Russell-Anelli J
"tir- and stx-Positive Escherichia coli in Stream Wat
                                                                                                                                                                                                                                                                                                                           STRAIN-Baisman's Run stream;
Hohn C., Karns J.S., Higgins J.A.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Metropolitan Area.";
Appl. Environ. Micro
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Enterobacteriaceae; Escher
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GO:0004872; F:receptor
GO:0007155; P:cell adhe
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STRAIN=95ZG1;
MEDLINE=99003184; PubMed=9784578;
Paton A.W., Manning P.A., Woodrow M.C., Paton J.C.;
"Translocated intimin receptors (Tir) of Shiga-toxigenic I coli isolates belonging to serogroups O26, O111, and O157
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Pfam; PF03549; Tir_receptor_M;
Pfam; PF073490; Tir_receptor_N;
PRINTS; PR01370; TRNSINTIMINR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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"EspE, a novel secreted protein of attaching and effacing bacter
directly translocated into infected host cells where it appears
tyrosine-phosphorylated 90 kbs/protein.";
Mol. Microbiol. 28:463-474(1998).
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DOI=10.1128/IAI.68.4.2171-2182.2000;
Marches O., Nougayrede J.-P., Boullier S., Mainil J., Charlier G.,
Raymond I., Pohl P., Boury M., De Rycke J., Milon A., Oswald E.;
"Role of tir and intimin in the virulence of rabbit enteropathogenic Escherichia coli serotype 0103:H2.";
Infect. Immun. 68:2171-2182(2000).
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STRAIN=413/89-1;
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(R; Q47014; 261-325.

Q; G0:0004872; F:receptor activity; IF
Q; G0:0007125; P:cell adhesion; IEA.

InterPro; IPR003536; Tir_rcpt.

IRCORD Tir_rcpt.

IRCORD Tir_rcpt.
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heterogeneity.";
Immun. 66:5580-5586(1998).
AGLIGMAATGIAQAVALTPEPDDPITTDPDAAANTAEAAAKDQLTKEAFQNPDNQKVNID
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RL Submitted (DEC
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RP NUCLEOTIDE SEC
RC STRAIM-REPEC 8
RA Krejany E.O.;
RL Submitted (WAH
RN [3]
RP NUCLEOTIDE SEC
RC STRAIM-RDEC-1;
RX MEDLINE-982541
RA Jain T.S., Boe
RI [4]
RP NUCLEOTIDE SEC
RC STRAIM-RDEC-1;
RX MEDLINE-982541
RA Lai L.C., MCNE
RT "The complete
RT From enteropat
RN [4]
RP NUCLEOTIDE SEC
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RX MEDLINE-993541
RA Lai L.C., MCNE
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RT MEDLINE-90351
RA Jain T.S., Cai
RT STRAIM-RDEC-1;
RX MEDLINE-91051
RN [5]
RP NUCLEOTIDE SEC
RC STRAIM-RDEC-1;
RX MEDLINE-911531
RX MEDLINE-211531
RX MEDLINE-21153/II
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RX DOI-010.1128/II
RA Zhu C., Agin T.
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NUCLEOTIDE SEQUENCE.
STRAIN-EDEC-1;
MEDLINE-21133569; PubM
DOI=10.1128/TAI.69.4.2
Zhu C., Agin T.S., Ell
                                                                                                                   MEDLINE=97055784; PubMed=8900070; DOI=10.1016/0378-1097(96)0037 Agin T.S., Cantey J.R., Boedeker E.C., Wolf M.K.; "Characterization of the eaeA gene from rabbit enteropathogenic Escherichia coli strain RDEC-1 and comparison to other eaeA gene bacteria that cause attaching-effacing land."
                                                                                                                                                                                                                                                        Elliott S.J., Wainwright L.A., McDaniel T.K., Jarvis K.G., De Lai L.C., McNamara B.P., Donnenberg M.S., Kaper J.B.; Lai L.C., mcNamara B.P., Donnenberg M.S., Kaper J.B.; "The complete sequence of the locus of enterocyte effacement from enteropathogenic Escherichia coli E2348/69."; mol. Microbiol. 28:1-4(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=RDEC-1;
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l. Lett. 144:249-258(1996).
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     Johnson
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3.C., Wolf M.K.;
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15-FEB-2005,

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                                                                                                                                                                       Receptor.
SEQUENCE
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"Description of a 111-kb pathogenicity island (PAI) encoding various virulence features in the enterchemorrhagic E. coli (BHEC) strain RW1374 (Ol03:H2) and detection of a similar PAI in other EHEC strains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22522600; PubMed=12635929;
Rumer L., Jores J., Kirsch P., Cavignac Y., Zehmke K., Wieler
"Dissemination of pheU and pheV located genomic islands among
enteropathogenic (EPEC) and enterohemorrhagic (EHEC) E. coli
possible role in the horizontal transfer of the locus of enter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RW1374 (O103:H2) and detection of serotype O103:H2.";
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SMR; Q58189; 261-325.

SMR; Q58189; 261-325.

GO; GO:0004872; F:receptor activity;

GO; GO:0007155; P:cell adhesion; IEA

InterPro; IPR003536; Tir rept.

Pfam; PF07489; Tir_receptor_C; 1.

Pfam; PF03549; Tir_receptor_M; 1.
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PubMed=15870341; DOI=10.1118/AEM.71.5.2511-2519.2005;
Higgins J.A., Belt K.T., Karns J.S., Russell-Anelli J., S
"tir- and stx-Positive Escherichia coli in Stream Waters
Metropolitan Area.";
                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=183192;
                                                                                                                 EMBL; AY944736; AAX47729.1;
                                                                                                                                                   Distributed under the Creative
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                                                                                                                                                                                                                                           STRAIN=Gywnns Run
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Shelton D.R., Higgins J.A.;
d (FEB-2005) to the EMBL/GenBank/DDBJ databases.
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Attribution-NoDerivs License
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                      MEDLINE=99003184; PubMed=9784578; Paton A.W., Manning P.A., Woodrow M.C., Paton J.C.; Paton A.W., Manning P.A., Woodrow M.C., Paton J.C.; "Translocated intimin receptors (Tir) of Shiga-toxigenic Escherichia coli isolates belonging to serogroups 026, 0111, and 0157 react with sera from patients with hemolytic-uremic syndrome and exhibit marked sequence heterogeneity.";
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Pfam; PF03549; Tir_receptor_M; 1.
Pfam; PF07490; Tir_receptor_N; 1.
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GO; GO:0004872; F:receptor activity;
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR003536; Tir_rcpt.
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Hohn C., Karns J.S.,
Submitted (FEB-2005)
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GO; GO:0004872; F:receptor activity; IE
GO; GO:0004872; F:receptor activity; IEA.
InterPro; IPR003536; Tir rcpt.
Pfam; PF07489; Tir receptor G; 1.
Pfam; PF07549; Tir receptor M; 1.
Pfam; PF07490; Tir receptor N; 1.
PRINTS; PR01370; TRNSINTIMINR.
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PubMed=15870341; DOI-10.1128/AEM.71.5.2511-2519.2005;
Higgins J.A., Belt K.T., Karns J.S., Russell-Anelli J., Shelton "tir- and stx-Positive Escherichia coli in Stream Waters in a Metropolitan Area.";
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Pred. No. 2.4e-88;
2; Mismatches 103
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26-APR-2005,
26-APR-2005,
07-FEB-2006,
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Pfam; PF03549; Tir receptor M; 1.
Pfam; PF07490; Tir receptor N; 1.
PRINTS; PR01370; TRNSINTIMINR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Spring Branch stream;
Hohn C., Shelton D.R., Higgins J.A.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=Spring Branch stream;
PubMed=15870341; DOI=10.1128/AEM.71.5.2511-2519.2005;
Higgins J.A., Belt K.T., Karns J.S., Russell-Anelli J., S
"tir- and stx-Positive Escherichia coli in Stream Waters
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Enterobacteriaceae; Escherichia.
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                                                                            ENGNAI PSGELIDDVVAQIAEQAKAAGEQARQEAIESNSQAQKKYDEQHAKREQEMALSS
                                                                                                             ELGNAIPSGYLKDDVVANIEEQAKAAGEEAKQQAIENNAQAQKKYDEQQAKRQEELKVSS
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Pred. No. 2.4e-88;
0; Mismatches 105;
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RESULT 13
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MEDLINE=98187918; PubMed=9529069;
Voss E., Paton A.W., Manning P.A., Paton J.C.;
"Molecular analysis of Shiga toxigenic Escherichia coli"
"Molecular analysis of Shiga toxigenic matterits with hemoly
                                                                                                                                                                                                                                                                                                                                                                         Pfam, PF07489; Tir receptor C; Pfam, PF03549; Tir receptor M; Pfam, PF07499; Tir receptor N; Pfam; PF07499; Tir receptor N; PRINTS; PR01370; TRNSINTIMINR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Paton A.W., Manning P.A., Woodrow M.C., Paton J.C.; "Translocated intimin receptors (Tir) of Shiga-toxigenic Escherichia coli isolates belonging to serogroups O26, O111, and O157 react with sera from patients with hemolytic-uremic syndrome and exhibit marked sequence heterogeneity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins which react with sera from syndrome.";
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MEDLINE=99003184; PubMed=9784578;
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Enterobacteriaceae; Escherichia.
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07-FEB-2006,
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                                                  GDNRASDVPGLPVNPMRL--AASEITLNDGFEVLHDHGPLDTLNRQIGSSVFRVETQEDG
                                                                                                       MPIGNLGNNVNSNNLIPPAPPLPSQTDGASRGGAGQLINSTGALGSRLLFSPLRNSIADS
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ilarity 60.8%;
Conservative 68
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-DIPGLPVHPSRLATATSEICLLGGFEVLHDKGPLDTLNKQIGASAFRIEQQSDG
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STRAIN=CPG121;
PubMed=16272509; DOI=10.1128/JCM.43.11.5715-5720.2005;
Parmendia J., Ren Z., Tennant S., Midolli Viera M.A., Chon Garmendia J., Ren Z., Dahan S., Sircili M.P., Franzolin Whale A., Azzopardi K., Dahan S., Sircili M.P., Franzolin Trahvilai L.R., Phillips A., Gomes T.A., Xu J., Robins-Brow
                       Interpro; IPRO03536; Tir_rcpt.
Pfam; PF07489; Tir_receptor_C;
Pfam; PF03549; Tir_receptor_N;
Pfam; PF07490; Tir_receptor_N;
PRINTS; PR01370; TRNSINTIMINR.
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Enteropathogenic Escherichia coli Isolates.";
J. Clin. Microbiol. 43:5715-5720(2005).
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                                                                                                               EMBL; DQ007023; AAY25394.1; SMR; Q4ZIM1; 272-336.
                                                                                                                                                    Distributed under the Creative
                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Escherichia.
                                                                                    GO:0004872; F:receptor activity; GO:0007155; P:cell adhesion; IEA
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              HDMGGLTGGSNSAVNTSNNPPAPGSHRF
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                                    PARQAEEHIYDEVAADP-NYSVIQNFSGNNQVTG
                                                                         TGGNTPAQGGTDAIRAEDTSLNRRDSQRSTASTHWSDTSS--AVVNPYAEVGEARNSS--
                                                     PTSNSNTSVQNMGNTDSVVYSTIQHPPRDTTDNGARLLGNPSAGIQSTYARLA-LSGGLR
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07-JUN-2005,
07-FEB-2006,
                                                                                                                                                    "Distribution of tccP in Clinical Ente
Enteropathogenic Escherichia coli Isol
J. Clin. Microbiol. 43:5715-5720(2005)
                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.

STRAIN=CPG124-WC416, and CPG123-G58;

PubMed=16272509; DOI=10.1128/JCM.43.11.5715-5720.2005;

PubMed=16272509; DOI=10.1128/JCM.43.11.5715-5720.2005;

Garmendia J., Ren Z., Tennant S., Midolli Viera M.A., Chong Y

Whale A., Azzopardi K., Dahan S., Sircili M.P., Franzolin M.F

Whale A., Azzopardi K., Dahan S., Sircili M.P., Robins-Browne
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EMBL; DQ007022; AAY25393.1; -; Genomic_DNA.
SMR; Q4ZIM0; 272-336.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
InterPro; IPR003538; Tir_rept.
Pfam; PF07499; Tir_receptor_C; 1.
Pfam; PF07499; Tir_receptor_N; 1.
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The invention relates to a novel enterohaemorragic Escherichia coli 0157:H7-specific nucleic acid molecule. A polynucleotide of the invention has anti-bacterial activity. The polypeptide can be used in detection and/or treatment of 0157:H7 infection. The nucleotide sequence of the genome of Enterohaemorragic E coli 0157:H7 was determined. The present sequence represents an E. coli 0157:H7-specific polypeptide of the
                                                                                        Enterohemorragic Escherichia coli 0157:H7-specific nucleic and a polypeptide and its use, a polypeptide, a vector and
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Ady52374
Ady51371
Abb71737
Abb63003
Abb65941
Abj05379
Adf49209
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Adm98799
Adm98789
Adm98937
Adm98827
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Ads44712
Ada17078
Ada17079
Abb59914
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Aae02560
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Sequence 558

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Best Local Sim:
Matches 558;
                                                                                                                                             bordetella pertussis infection; antibacterial; pneumonia, antiinflammatory; respiratory-gen.; gastric ulcer; antiul gastrointestinal-gen.; urinary tract infection; antimicro
                      06-FEB-2004;
20-JUL-2004;
                                                                                                                                                                                                  Microbial pathogen
                                                                                                                                                                                                                                               AEB91310;
                                                       07-FEB-2005;
                                                                                                                        Escherichia coli.
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(COUL ) COUNCIL SCI & IND RES
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                      2004IN-DE000173.
2004US-0589227P.
                                                       2005WO-IN000037.
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                                                                                                                                                                                                                                                                    protein;
                                                                                                                                                                             pharmaceutical; vaccine; drug
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The present invention relates to a computational method (MI) for clidentifying adhesin and adhesin-like proteins, by computing the sequence based attributes of protein sequences using five attribute modules of a neural network software, training an artificial neural network (ANN) for ceach of the computed five attributes, and identifying the adhesin and cadhesin-like proteins having probability of being an adhesin (Pad) as cerocoding adhesin and adhesin-like proteins, having 274 fully defined 162-cerocoding adhesin and adhesin-like proteins, having 274 fully defined 162-cerocoding adhesin and adhesin-like proteins, having 105 fully defined 306-15876 base pairs (SEQ ID NO: 659-763); a set of 1279 annotated cadhesin and adhesin-like proteins, having 105 fully defined 30-3716 base pair (SEQ ID NO: 1279); a set of 105 hypothetical adhesin and adhesin-like proteins, having 279 fully defined 33-3716 base pair (SEQ ID NO: 1279); a set of 105 hypothetical adhesin and adhesin-like proteins, having 279 fully defined 53-3716 base pair (SEQ ID NO: 1279); a set of 105 hypothetical adhesin and adhesin-like proteins, having 279 fully defined 53-3716 base pair (SEQ ID NO: 1279); a set of 105 hypothetical adhesin and adhesin-like proteins, having 105 fully connected multilayer feed forward ANN (I) based on (M1). (M1) is useful for identifying adhesin and adhesin-like proteins, of therapeutic potential, and identifying and short-listing conceins for further testing in development of new vaccine formulations to eliminate diseases caused by various pathogenic organisms. (M1) is useful for identifying and short-listing conceins for further testing in development of new vaccine formulations to eliminate diseases caused by various pathogenic organisms, (M1) is capable of proteins bequence of a wide of pathogenetic spectrum. (M1) is capable of predicting adhesive nature of unique proteins. The present sequence is a microbial pathogen adhesin
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Best Local :
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Best Local Similarity 100 Matches 558; Conservative

100.0%; So 100.0%; Po ative 0;

Score 558; D Pred. No. 0; 0; Mismatches

BG 10; 0

Length Indels

558; 0

Gaps

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Query Match

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                                            CC The present invention relates to novel EspFU polypeptides and their CC corresponding polynucleotides. The EspFU polypeptides are EspF-like CC polypeptides encoded by genes of the cryptic prophage CP-93JU of CC enterohemorrhagic Escherichia coli (EHEC) or enteropathogenic Escherichia coli (EPEC) that binds to a neuronal wiskott-aldrich syndrome protein (N-CC WASP) polypeptide or restores the actin pedestal formation activity of enteropathogenic E. coli (EPEC) strain KC12. The invention further CC relates to a method of identifying a candidate compounds capable of binding to and/or modulating the activity of EspFU and compounds that CC binding to and/or modulating the activity of EspFU and EspFU-interacting proteins such as N-WASP, transducer of Cdc42-dependent actin assembly-1 (Toca-1) and p21-activated kinase 1 (Pakl). EspFU polynucleotides are useful for treating EHEC infection. EspFU antibody is useful for treating EHEC infection. The present sequence is the conterohemorrhagic Escherichia coli translocated intimin receptor (Tir) protein. This sequence is critical for the formation of actin pedestals
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 Sequence
                                                                                                                                                                                                                                                                                                                                                                              Novel purified polypeptide having six residues of EspF-U, and binding neuronal Wiskott-Aldrich syndrome protein polypeptide, useful for identifying EspF-U activity modulating compound.
                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 12; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2006-065745/07.
N-PSDB; AEE86219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Leong JM, Campellone
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(CAMP/) CAMPELLONE K G.
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causing frameshift in the DNA sequence"
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Best Local S
Matches 452
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                         NVDTPGSEDTMESRRSSMASTSSTFFDTSSIG 452
                                                                                                  AGYGLSGALILGGGIGVAVTAALHRKNQPVEQTTTTTTTTTTTTSARTVENKPANNTPAQG
                                                                                                                                                                        LGNAI PSGVLKDDVVANI EEQAKAAGEEAKQQAI ENNAQAQKKYDEQQAKRQEELKVSSG
                                                                                                                                                                                                                                              GLIGLAATGIVQALALTPEPDSPTTTDPDAAASATETATRDQLTKEAFQNPDNQKVNIDE
                                                                                                                                                                                                                                                                                                                       ELLEPKGTGESKGAGESKGVGELRESNSGAENTTETQTSTSTSSLRSDPKLWLALGTVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NRASDVPGLPVNPMRLAASEITLINDGFEVLHDHGPLDTLINRQIGSSVFRVETQEDGKHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NRASDVPGLPVNPMRLAASEITLNDGFEVLHDHGPLDTLNRQIGSSVFRVETQEDGKHIA
                                                                                                                                                                                                                          GLIGLAATGIVQALALTPEPDSPTTTDPDAAASATETATRDQLTKEAFQNPDNQKVNIDE
                                                                                                                                                                                                                                                                                                  ELLEPKGTGESKGAGESKGVGELRESNSGAENTTETQTSTSTSSLRSDPKLWLALGTVAT
                                                                                                                                                                                                                                                                                                                                                                          VGQRNGVETSVVLSDQEYARLQSIDPEGKDKFVFTGGRGGAGHAMVTVASDITEARQRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MPIGNLGHNPNVNNSIPPAPPLPSQTDGAGGRGQLINSTGPLGSRALFTPVRNSMADSGD
                                                                         AGYGLSGALILGGGIGVAVTAALHRKNQPVEQTTTTTTTTTTTTSARTVENKPANNTPAQG
                                                                                                                                                 LGNAIPSGVLKDDVVANIEEQAKAAGEEAKQQAIENNAQAQKKYDEQQAKRQEELKVSSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.0%;
ilarity 100.0%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 452; D
Pred. No. 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
   452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 559;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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16-AUG-1999

(first entry)

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RESULT 6
AAY06220
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                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents the N-terminal sequence of Tir (see also AAY06220), a novel translocated intimin receptor from an enteropathogenic Escherichia coli (EPEC) strain. The 78 Me EPEC protein is secreted by the bacterial pathogen. Diagnosis of disease caused by pathogenic E coli can be performed by use of antibodies that bind to Tir to detect the protein, or the use of nucleic acid probes for detection of nucleic acids encoding Tir. A kit for the detection of Tir-producing E. coli is provided. Also provided are a method of immunising a host with Tir to induce a protective immune response, and a method for screening for compounds which interfere with the binding of bacterial pathogens to
               Misc-difference
                                                   Location/Qualifiers
                                                                                                     Escherichia
                                                                                                                         Tir; translocated intimin receptor; Hp90; enteropathogenic; EPEC; infection; diagnosis; vaccine.
                                                                                                                                                                  EPEC E.
                                                                                                                                                                                           16-AUG-1999
                                                                                                                                                                                                                   AAY06220;
                                                                                                                                                                                                                                           AAY06220 standard; protein; 549
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 30 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                      their receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New translocated intimin receptor useful for treating infection enteropathogenic or enterohemorrhagic Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 37; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-337712/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Finlay BB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09924576-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tir; translocated intimin receptor; Hp90; enteropathogenic; EPEC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYBR-) UNIV BRITISH COLUMBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              infection; diagnosis; vaccine
                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
H
                                                                                                                                                                                                                                                                                                                                     16
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                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                 coli translocated intimin receptor (Tir).
                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 coli translocated intimin receptor N-terminal peptide
                                                                                                                                                                                                                                                                                                            IPPAPPLPSOTDGA 28
                                                                                                                                                                                                                                                                                                                                  IPPAPPLPSQTDGA 29
                                                                                                    coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kenny B,
                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0065130P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-CA001042
/note= "given as Xaa in the specification; Lys is deduced
                          'note= "putative transmembrane domain"
                                                  note= "encoded by
                                                                                                                                                                                                                                                                                                                                                       2.5%; 500
100.0%; Pr
                                       . 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Devinney R,
                                                                                                                                                                                                                                                                                                                                                                        Score 14;
Pred. No.
                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                  AAA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Stein M;
                                                                                                                                                                                                                                                                                                                                                          1.9e-05;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                  Length 30
                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                          Gaps
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RESULT 7
AEE26469
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Best Local S
Matches 14
                                                                                      Vaccine; Gene-therapy; Staphylococcus aureus;
                                                                                                                                                                     09-FEB-2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to detect the protein or the use of nucleic acid probes for detection of nucleic acids encoding Tir polypeptide. Isolated Tir nucleic acids, Tir peptides, a recombinant method for producing recombinant Tir, antibodies which bind to Tir, and a kit for the detection of Tir-producing E. coli are provided. A method of immunising a host with Tir to induce a protective immune response is also provided. In addition, Tir fusion protective immune response is also provided. In addition, Tir fusion protecting can be used in attenuated E. coli to induce a cell-mediated immune response to other polypeptides, e.g. antigens. A method for screening for compounds which interfere with the binding of bacterial
             WO2005115113-A2
                                                         Staphylococcus aureus;
                                                                                                                                     ORF0826 immunogen related
                                                                                                                                                                                                    AEE26469;
                                                                                                                                                                                                                               AEE26469 standard; protein; 162 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          effacing pathogens such as EPEC and EHEC (see AAY06221) E. coli. The bacterial pathogens insert their own receptors into mammalian cell surfaces, to which the pathogen then adheres to trigger additional host signaling events and actin nucleation. Diagnosis of disease caused by pathogenic E. coli can be performed by use of antibodies that bind to Tir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents Tir, a novel translocated intimin receptor (formerly termed Hp90) from an enteropathogenic Escherichia c(EPEC) strain. The sequence was deduced from an isolated tir polynucleotide (see AAX58858). Tir proteins are secreted by attaching
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pathogens to their
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New translocated intimin receptor useful for treating infection enteropathogenic or enterohemorrhagic Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 55-58; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-337712/28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Finlay BB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYBR-) UNIV BRITISH
                                                                                                                                                                                                                                                                                                              16
                                                                                                                                                                                                                                                                                                                                           16 IPPAPPLPSQTDGA 29
                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          549
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                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from the DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    receptors is further provided
                                                                                                                                                                                                                                                                                                                                                                                       2.5%;
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                                                       methicillin resistant strain
                                                                                      Antibacterial; immunogen; ORF0826; Ssa; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "putative transmembrane domain"
                                                                                                                                     sequence
                                                                                                                                                                                                                                                                                                                                                                         ; Score 14; DB
%; Pred. No. 0.0
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                       DB 2; L
                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                      Length 549;
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                         Gaps
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RESULT 8
ABJ18927
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-DEC-2005.
            WPI; 2003-075410/07
                                       Tempelmaier B;
                                                  Meinke A, Nagy E,
Minh DB, Vytvytska
                                                                                                                   26-JAN-2001; 2001AT-00000130
                                                                                                                                              21-JAN-2002; 2002WO-EP000546.
                                                                                                                                                                                                   WO200259148-A2
                                                                                                                                                                                                                            Staphylococcus sp.
                                                                                                                                                                                                                                                      autoimmune disease;
                                                                                                                                                                                                                                                                  Antibacterial; virucide; fungicide; protozoacide; cytostatic; anti-HIV, hyperimmune; serum-reactive; antigen; pathogen; tumour; allergen; auto-immunity; vaccine; staphylococcal infection; antibody; cancer;
                                                                                                                                                                                                                                                                                                                     Pathogen specific antigen related staphylococcal protein SEQ ID No 73.
                                                                                                                                                                                                                                                                                                                                                 06-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                   ABJ18927 standard; protein; 166 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This sequence represents a polypeptide related to the immunogen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; SEQ ID NO 3; 28pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                derivative of Staphylococcus aureus polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide immunogen useful for inducing protective immunity staphylococcus aureus comprises amino acid sequence, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2006-020409/02.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAY-2004; 2004US-0574032P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-MAY-2005; 2005WO-US017835.
                                                                                          (CIST-)
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nes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40
                                                                                          CISTEM BIOTECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QTTTTTTTTTTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QTTTTTTTTTTTS 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.3%; Score 13; DB llarity 100.0%; Pred. No. 0. Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention.
                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                     HIV;
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                                                                Von
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                                                  Etz H, [
                                                                                                                                                                                                                                                      hepatitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      English.
                                                                                          GMBH.
                                                   Dryla
                                                  Klade C,
Dryla A, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 10; I
0.00087;
                                                  , Henics T, Weichhart T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                  Zauner W;
Hafner M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            against; similar
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CC producing hyperimmune serum-reactive antigens from a pathogen, tumour, a tissue or host prone to auto-immunity, where the antigens are used in a vaccine, comprises providing antibody preparation from a plasma CC pool of a type of animal, or individual sera with antibodies against the immunity. The hyperimmune serum-reactive antigens comprising any of the cimunity. The hyperimmune serum-reactive antigens comprising any of the CC sequences of 53-2561 amino acids fully defined in the specification, or their hyperimmune fragments are useful for the manufacture of a CC or their hyperimmune fragments are useful for the manufacture of a CC infections or colonisation, particularly a vaccine against staphylococcal infections or colonisation against S. aureus or S. epidermidis. The CC preparation of antibodies is useful for the manufacture of a medicament CC for treating or preventing staphylococcal infections or colonisation cCC against S. aureus or S. epidermidis. The antibody preparations may also be used for diagnostic and imaging purposes. Other conditions that can be created include cancer, autoimmune diseases or infections caused by viral CC treated include cancer, autoimmune diseases or relating to the method for infections a staphylococcal protozoan pathogens. This capture felicity and account antibody preparation of the method for infections of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying, isolating and producing hyperimmune serum-reactive antigens from a pathogen, for preparing vaccine or medicament for treating or preventing e.g. staphylococcal infections, comprises providing antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel method for identifying,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 21; Page 157; 252pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isolating and
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Sequence 166 AA; ldentifying and producing pathogen specific antigens of the

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Matches
                                                 Query Match
Best Local Similarity
            392 QTTTTTTTTTTTTS 404
43 QTTTTTTTTTTS 55
                                        13;
                                        Conservative
                                                  2.3%;
                                         0;
                                                 Score 13; DB 6; I
Pred. No. 0.00089
                                         Mismatches
                                         <u>.</u>
                                         Indels
                                       0,
                                         Gaps
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Length 166

0

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RESULT 9
ABM71151
ID ABM7
 ABM71151 standard; protein; 166 AA
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20-NOV-2003 ABM71151; (first entry)

Staphylococcus aureus protein #391.

enzymatic assay; antibiotic target Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;

Staphylococcus aureus

28-NOV-2002

27-MAR-2002; 2002WO-IB002637.

27-MAR-2001; 2001GB-00007661

(CHIR-) CHIRON SPA

Masignani V, Mora M,

WPI; 2003-120786/11. ACF72711.

New Staphylococcus aureus preventing Staphylococcal S. aureus, e.g. sepsis. protein, useful as a vaccine for treating infection, specifically an infection cause an infection caused or R λq

Claim 1; SEQ ID NO 782; 49pp; English

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RESULT 10
AEE26470
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Best Local S
Matches 13
antigen Ssa. This immunogen can induce protective immunity against S. aureus. The immunogen can induce protective immunity against S. subcutaneously, intramuscularly or mucosally. It is used for inducing protective immunity against s. apatient e.g. human for treating prophylactically against Staphylococcus aureus infection. The polypept immunogen provides protective immunity against Staphylococcus aureus traphylococcus aureus. This sequence shares 85% homology to ORF0826 but is excluded from the scope of the invention.
                                                                                                                                                                                                            ORF0826
                                                                                                                                                                                                                                                                                    Example 1; SEQ ID NO 4; 28pp; English
                                                                                                                                                                                                                                                                                                                                         derivative
                                                                                                                                                                                                                                                                                                                                                      Polypeptide immunogen useful for inducing protective immunity against Staphylococcus aureus comprises amino acid sequence, which is similar
                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2006-020409/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anderson AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2004; 2004US-0574032P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vaccine; Gene-therapy; Antibacterial; immunogen; ORF0826; Ssa; Staphylococcus aureus; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORF0826 immunogen related sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel genes and encoded proteins from Staphylococcus aureus. A composition comprising the S. aureus protein, a nucleic acid encoding the protein, or an antibody to the protein, is useful as a pharmaceutical, particularly as a vaccine for treating or preventing infection due to Staphylococcus bacteria, specifically an infection caused by S. aureus. The composition is particularly useful for treating or preventing sepsis in a patient. The composition can also be used for diagnostics. The protein is also used in an assay for enzymatic studies and as a target for antibiotics. This sequence represents one of the novel S. aureus proteins of the invention
                                                                                                                                                                                                                                 This sequence represents a polypeptide related to the immunogen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEE26470 standard;
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                                                                                                                                                                                                         shares a high degree of
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                                                                                                                                                                                                                                                                                                                                    of Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aureus;
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Pred. No.
                                                                                                                                                                                                         homology with S. epidermis secreted
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                                                     polypeptide aureus.
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Query Match

2.3%;

Score

13;

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Length 166;

09-FEB-2006 AEE26472; AEE26472

(first entry)

RESULT 12 AEE26472 ID AEE26

standard;

protein;

166 AA

Sequence 166 AA;

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                                                                                                 RESULT 11
AEE26471
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Matches 13
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                                                                                                                      This sequence represents a polypeptide related to the immunogen, ORF08 ORF0826 shares a high degree of homology with S. epidermis secreted antigen Ssa. This immunogen can induce protective immunity against S. aureus. The immunogen is administered at a dosage of 1 microg-1 mg, subcutaneously, intramuscularly or mucosally. It is used for inducing protective immune response in a patient e.g. human for treating prophylactically against Staphylococcus aureus infection. The polypept immunogen provides protective immunity against Staphylococcus aureus. This sequence shares 85% homology to ORF0826 but is excluded from the scope of the invention.
                                                                                               Sequence 166
                                                                                                                                                                                                                                                                                      Polypeptide immunogen useful for inducing protective Staphylococcus aureus comprises amino acid sequence, derivative of Staphylococcus aureus polypeptide.
                                                                                                                                                                                                                                                                 Example 1; SEQ ID NO 5;
                                                                                                                                                                                                                                                                                                                                            WPI; 2006-020409/02.
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                                               ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aureus; methicillin resistant strain.
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55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Antibacterial; infection.
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                                                                                                                                                                                                                                                                28pp; English.
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                                                           Score 13;
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                                                Mismatches
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                                                           DB 10; 1
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Best Local S
Matches 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
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                                                                                                                                                                                                                                        Staphylococcus aureus
                                                                                                                                                                                                                                                                                                                                                                             ORF0826 immunogen.
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                                                                                                                                                                                                                                                                                          Staphylococcus
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                                                                                                                                                                                                                                                                                            Vaccine; Gene-therapy;
Staphylococcus aureus;
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coccus aureus;
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                                                                                                                                                                                                                                                                                               Antibacterial; immunogen; ORF0826; Ssa; infection.
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Matches 13
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                                                                                                                                                                                                                                                                                                                                         Vaccine; Gene-therapy; Staphylococcus aureus;
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                                                                               Polypeptide immunogen useful for inducing protective immunity against Staphylococcus aureus comprises amino acid sequence, which is similar derivative of Staphylococcus aureus polypeptide.
                                                                                                                                                                                                                                                                                                                  Staphylococcus aureus.
                                                                                                                                                                                                                                                                                                                                                                            Full length ORF0826 immunogen.
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                                                                                                                                 N-PSDB;
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mes 13; Conserv
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)B; AEE26475.
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                                                                                                                                                                                                                                                                                                                                                     Antibacterial;
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This sequence represents a polypeptide m from which the immunogen, ORF0826, is derived. ORF0826 shares a high degree of homology with S. epidermis secreted antigen Saa. This immunogen can induce protective immunity against S. aureus. The immunogen is administered at a dosage

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epidermis secreted a immunity against S.

Example

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                                                                                                                               The invention relates to a chitinase (I) comprising a chitin binding domain (D1) connected to a catalytically active domain (D2) comprising the 289 amino acid sequence of ABF20209, or ABF20209 in which one or more amino acids being deleted, substituted or added, through a direct or a connecting region. Also described: (1) a DNA (II) encoding (I); (2) a recombinant vector (III) containing (II); (3) a transformed host (IV) containing (IIII); and (4) producing (I). (I) is useful for hydrolyzing chitin. (I) exhibits high activity and stability, even at high temperature. The present sequence represents a Pyrococcus furiosus chitinase connection region amino acid sequence, which is given in the exemplification of the present invention.
                                                                                                           Sequence 81
                                                                                                                                                                                                                                                                                                     Claim 4; SEQ ID NO 6; 15pp; Japanese
                                                                                                                                                                                                                                                                                                                               Novel chitinase comprising a chitin binding domain connected to a catalytically active domain, through a direct or connecting region, useful for hydrolyzing chitin.
                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AEF20218.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l microg-1 mg, subcutaneously, intramuscularly or mucosally. It is used for inducing protective immune response in a patient e.g. human for treating prophylactically against Staphylococcus aureus infection. The polypeptide immunogen provides protective immunity against Staphylococcus
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| 00000000000                                                                                                                                                                                                                                                                                                                                                               | -09-248-7<br>-08-651-5<br>-09-066-5<br>-08-951-0<br>-09-248-7                                                                                                                                                                           | -09-248-796A-2584<br>-09-248-796A-2584<br>-09-248-796A-1623<br>-09-248-796A-1823<br>-09-248-796A-2921<br>-09-248-796A-2291<br>-09-270-767-41918<br>-09-287-796A-1899 | -09-248-7;<br>-09-248-7;<br>-09-248-7;<br>-09-248-7;<br>-09-248-7;<br>-09-248-7;<br>-09-248-7;<br>-09-248-7;<br>-09-248-7;                                                                                                                                                                                                                                                                                                    | -10-029-212-11<br>-09-248-796A-211<br>-09-248-796A-217<br>-09-248-796A-278<br>-09-248-796A-278<br>-09-513-99C-36<br>-09-513-99C-36<br>-09-270-767-3929<br>-09-270-767-3929<br>-09-248-796A-142<br>-09-248-796A-168<br>-09-248-796A-168<br>-09-248-796A-168<br>-09-248-796A-168<br>-09-248-796A-168<br>-09-248-796A-168 | US-09-248-796A-15978 US-09-252-991A-30886 US-09-260-767B-3 US-09-248-796A-15817 US-09-248-796A-20897 US-09-248-796A-16779 US-09-248-796A-22270 US-09-248-796A-14299 US-09-248-796A-14299 US-09-248-796A-14299 US-09-248-796A-15524 US-09-248-796A-15524 US-09-248-796A-15507 US-09-762-724-10 US-09-762-724-12 US-09-762-724-14                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |
| Sequence 2, Appli<br>Sequence 2, Appli<br>Sequence 2, Appli<br>Sequence 1, Appli<br>Sequence 1, Appli<br>Sequence 60233, A<br>Sequence 5, Appli<br>Sequence 5, Appli<br>Sequence 7, Appli<br>Sequence 7, Appli                                                                                                                                                            | equence 2, equence 2, equence 2, equence 2, equence 2, equence 2, equence 205 equence 205 equence 205 equence 205                                                                                                                       | equence 258 equence 258 equence 163 equence 183 equence 229 equence 229 equence 415 equence 415 equence 616                                                          | equence 187 equence 219 equence 153 equence 187 equence 187 equence 179 equence 240 equence 240 equence 217 equence 218 equence 218 equence 218 equence 222                                                                                                                                                                                                                                                                   | 1168<br>1168<br>1168<br>1168<br>1168<br>1168<br>1168<br>1168                                                                                                                                                                                                                                                           | Sequence 15978, A Sequence 3, Appli Sequence 3, Appli Sequence 15817, A Sequence 14897, A Sequence 14994, A Sequence 22220, A Sequence 22277, A Sequence 22277, A Sequence 14299, A Sequence 14524, A Sequence 14524, A Sequence 15507, A Sequence 15453, A Sequence 174, Appl Sequence 12, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 14, Appl Sequence 16, Appl                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
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GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO AG
TITLE OF INVENTION: FOR DIAGNOSTICS AND THEE
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
 RESULT 2
US-09-248-796A-25055
; Sequence 25055, Application US/09248796A
; Patent No. 6747137
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 US-09-248-796A-17879
 US-09-248-796A-17879
 PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 17879
LENGTH: 160
 Sequence 17879, Application US/09248796A Patent No. 6747137 GENERAL INFORMATION:
 Matches
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Best Local
 APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
 ORGANISM: Candida albicans
 TYPE: PRT
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US-09-236-115C-10

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US-09-949-016-7806

US-09-949-016-7806

US-09-185-160-11

US-09-824-574-6

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US-10-1140-047-1975

US-10-105-364-45

US-09-6349A-6

US-09-949-016-9522

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 Score 12;
Pred. No.
 US-09-248-796A-19273
US-10-087-167-137
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PRIOR APPLICATION NUMBER: US 60/096,409
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PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
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 US-09-248-796A-22880
 US-09-248-796A-18318
 RESULT 3
US-09-248-796A-18318
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 PATENT NO. 6747137

GENERAL INFORMATION:
APPLICANT: Keith Weinstock et al
APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: WCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-13
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
 US-09-248-796A-25055
 NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 18318
LENGTH: 541
 GENERAL INFORMATION:
 Sequence 22880, Application US/09248796A Patent No. 6747137
 PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 25055
 Matches
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 Query Match
 Matches
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 Query Match
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 NAME/KEY: UNSURE
LOCATION: (287), (288), (289)
OTHER INFORMATION: Identity of amino
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TYPE: PRT
ORGANISM: Candida albicans
FEATURE:
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 Local
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 393 TTTTTTTTTTTS 404
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 12;
 Similarity
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 US/09248796A
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Pred. No.
 Score 12;
Pred. No.
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 Mismatches
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 DB 2;
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 Length 292;
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 Gaps
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ORGANISM: Candida albicans

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 ; NAME/KEY: UNSURE
; LOCATION: (667)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
US-09-248-796A-22880
 US-10-037-417-48
NUMBER OF SEQ ID NOS: 227
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 48
LENGTH: 3712
TYPE: DDm
 Sequence
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 Query Match
 Patent No.
 FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR FILING DATE: 2001-01-05
 APPLICANT:
 APPLICANT:
APPLICANT:
 TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same FILE REFERENCE: 21402-235
 APPLICANT: Kekuda, Ramesh
 PRIOR FILING DATE:
 PRIOR APPLICATION NUMBER: 60/305,060
 PRIOR FILING DATE:
 PRIOR APPLICATION NUMBER: 60/272,817
 PRIOR APPLICATION NUMBER: 60/260,360 PRIOR FILING DATE: 2001-01-08
 APPLICANT:
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 PRIOR APPLICATION NUMBER: 60/318,700
 APPLICANT
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 FEATURE:
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 FILING DATE:
 APPLICATION NUMBER: 60/272,411
 APPLICATION NUMBER: 60/291,186
 APPLICATION NUMBER: 60/303,231
 FILING DATE:
 FILING DATE:
 APPLICATION NUMBER: 60/318,405
 585
 INFORMATION:
 393
 48,
 TTTTTTTTTTTS 404
 TTTTTTTTTTS 596
 Taupier Jr, Raymond J
Miller, Charles E
Eisen, Andrew J
 Lepley, Denise M
 Application US/10037417
 Alsobrook II, John I
Tchernev, Velizar T
 Rothenberg, Mark
Stone, David J
 Edinger, Shl
 Anderson, David W
Padigaru, Muralidhara
 Shenoy, Suresh G
 Boldog, Ferenc L
Guo, Xiaojia
 Malyankar, Uriel M
 Gorman, Linda
 Burgess,
 Patturajan, Meera
Grosse, William M
 Spytek, Kimberly A
 Conservative
 lerman, Karen
 Xiaohong
 2001-07-12
 2001-09-10
 2001-07-05
 2001-05-15
 2001-02-28
 Corine A.M
 Catherine E
 2.2%; Score 12; DB 2; Length 667; 100.0%; Pred. No. 0.013;
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 Mismatches
 0
 Indels
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 Gaps
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RESULT 6
US-10-037-417-51
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 ; ORGANISM: Drosophila melanogaster US-10-037-417-48
 FILE REFERENCE: 21402-235
CURRENT APPLICATION NUMBER: US/10/037,417
CURRENT FILING DATE: 2002-09-20
PRIOR APPLICATION NUMBER: 60/260,018
PRIOR FILING DATE: 2001-01-05
PRIOR PRICING DATE: 2001-01-08
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PRIOR FILING DATE: 2001-03-08
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PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
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Matches 12; Conserv
 SEQ ID NO 51
LENGTH: 3712
 Sequence
 Patent No.
 APPLICANT:
 APPLICANT:
 APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT:
 APPLICANT: Kekuda, Ramesh
APPLICANT: Alsobrook II, Johr
APPLICANT: Tchernev, Velizar
 NUMBER OF SEQ ID NOS: 227
SOFTWARE: PatentIn Ver. 2
 PRIOR APPLICATION NUMBER: 60/318,405
PRIOR FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: 60/318,700
PRIOR FILING DATE: 2001-09-12
 PRIOR FILING DATE: 2001-05-15
PRIOR APPLICATION NUMBER: 60/303,231
PRIOR FILING DATE: 2001-07-05
 APPLICANT: Taupier Jr, Raymond J
APPLICANT: Miller, Charles E
APPLICANT: Elsen, Andrew J
TITLE OF INVENTION: Proteins and Nucleic Acids Encoding
 APPLICANT:
 PRIOR APPLICATION NUMBER: 60/305,060 PRIOR FILING DATE: 2001-07-12
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 APPLICANT
 APPLICANT:
ORGANISM: Drosophila melanogaster
 TYPE: PRT
 APPLICATION NUMBER: 60/291,186
 3273 TTTTTTTTTTS 3284
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 INFORMATION:
 51, Application US/10037417
o. 6903201
 PatentIn Ver. 2.1
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 Malyankar, Uriel M
Rothenberg, Mark
Stone, David J
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Padigaru, Muralidhara
 Shenoy, Suresh G
 Boldog, Ferenc L
Guo, Xiaojia
 Edinger, Shi
Sciore, Paul
 Gorman, Linda
 Patturajan, Meera
Grosse, William M
 Spytek,
 Ellerman, Karen
 Vernet,
 Lepley, Denise M
 Liu, Xiaohong
 2.2%; Score 12; larity 100.0%; Pred. No. Conservative 0; Mismatc
 Kimberly A
 Corine A.M.
 Shlomit R
 Catherine
 John
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 Mismatches
 DB 2;
0.067;
 Length 3712;
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 Query Match
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 ; ORGANISM: Human US-09-949-016-6978
 US-09-949-016-6978
 ; ORGANISM: Human US-09-949-016-10933
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 US-09-949-016-10933
 ঠ
 Sequence 6978, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION UNMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
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Best Local Similarity
Matches 12; Conserv
 NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 6978
LENGTH: 4377
 NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10933
LENGTH: 3913
 GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 Sequence 10933, Application US/09949016 Patent No. 6812339
 Matches
 FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03
 PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
 PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
 TYPE: PRT
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 393 TTTTTTTTTTTS 404
 393 TITTTTTTTTS 404
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Conservative (
 ilarity 100.0%; E Conservative 0;
 Conservative
 100.0%;
 2.2%; Score 12; DB 2;
L00.0%; Pred. No. 0.078;
 2.2%; Score 12; DB 2; 00.0%; Pred. No. 0.07;
 2.2%; Score 12; DB 2; 100.0%; Pred. No. 0.067;
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 Mismatches
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 DB 2; Length 3712;
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 Length 3913;
 Length 4377;
 Indels
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 US-09-060-767B-5
 RESULT 10
US-09-060-767B-5
 RESULT 9
US-10-029-212-10
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 US-10-029-212-10
 GENERAL INFORMATION:
APPLICANT: Weil, Gary
APPLICANT: Weil, Chandrashekar, Ramaswamy
APPLICANT: Chandrashekar, Ramaswamy
TITLE OF INVENTION: Diagnosis of Histoplasmosis Using Antigens Specific for
TITLE OF INVENTION: H. capsulatum
FILE REFERENCE: BüCH 9986
CURRENT APPLICATION NUMBER: US/09/060,767B
CURRENT APPLICATION NUMBER: 60/043,332
PRIOR APPLICATION NUMBER: 60/043,332
PRIOR FILING DATE: 1997-04-15
PRIOR FILING DATE: 1997-04-15
RUMBER OF SEQ ID NOS: 9
 SOFTWARE: PatentIn version 3.0 SEQ ID NO 5
 GENERAL INFORMATION:
APPLICANT: IMANISHI, Takeshi
APPLICANT: OBIKA, Satoshi
 Matches
 Query Match
Best Local Similarity
 Sequence 5, Application US/09060767B Patent No. 6720152
 SOFTWARE: PatentIn version 3.2 SEQ ID NO 10
 Query Match
Best Local Similarity
 Sequence 10, Application US/10029212
Patent No. 6770748
 Matches
 APPLICANT: OBIKA, Satoshi
TITLE OF INVENTION: NOVEL BICYCLONUCLEOSIDE AND OLIGONUCLEOTIDE ANALOGUE
FILE REFERENCE: IMANISHI 2B
CURRENT APPLICATION NUMBER: US/10/029,212
CURRENT FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: 09/904,567
PRIOR PILING DATE: 2001-07-17
PRIOR PILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: 09/380,638
PRIOR APPLICATION NUMBER: 09/380,638
PRIOR FILING DATE: 1999-09-07
PRIOR APPLICATION NUMBER: PCT/JP98/00945
PRIOR FILING DATE: 1998-03-09
NUMBER: OF SEQ ID NOS: 12
 LENGTH: 41
TYPE: PRT
ORGANISM: Leishmania
 TYPE: PRT
ORGANISM: Artificial
 OTHER INFORMATION: synthetic
 FEATURE:
 LENGTH: 13
 3968
393 TITTTTTTTT 403
 393 TTTTTTTTT 403
 11;
 2 TTTTTTTTTT 12
 Tritriritis 3979
 Conservative
 Conservative
 100.0%;
 2.0%; Score 11;
100.0%; Pred. No.
 Score 11; DB 2; L; Pred. No. 0.0083; 0; Mismatches 0;
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RESULT 11 US-08-900-230-59

Sequence 59,

9, Application US/08900230 6329197

No.

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 RESULT 12
US-09-248-796A-23083
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 US-09-248-796A-23083
 ; ANTI-SENSE:
US-08-900-230-59
 Sequence 23083, Application US/09248796A Patent No. 6747137
 Query Match
 SEQ ID NO 23083
LENGTH: 63
 GENERAL INFORMATION:
 APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
 PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
 GENERAL INFORMATION:
 NUMBER OF SEQ ID NOS: 28208
 TELEPHONE: 212-278-0400
TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 9
 TYPE: PRT
ORGANISM: Candida albicans
 MOLECULE TYPE:
HYPOTHETICAL:
 SEQUENCE CHARACTERISTICS:
LENGTH: 57 amino acids
TYPE: amino acid
STRANDEDNESS: single
 ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
 TITLE OF INVENTION:
 TELECOMMUNICATION INFORMATION:
 APPLICANT:
 CORRESPONDENCE ADDRESS
 NUMBER OF SEQUENCES:
 APPLICATION NUMBER: US/08/900,230 FILING DATE: 23-JUL-1997 CLASSIFICATION: 435
 CITY: New York
STATE: New York
 REFERENCE/DOCKET NUMBER:
 COUNTRY: U.S.A.
 STREET:
 TOPOLOGY:
 ADDRESSEE:
 393
 11036
 TTTTTTTTTT 403
 TTTTTTTTTT 11
 E: Cooper & Dunham LLp
1185 Avenue of The Americas
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 Jonathan A.
N: DNA ENCODING GALANN GALR3 RECEPTORS
 2.0%; Score 11; DB 2; Length 57; 100.0%; Pred. No. 0.011;
 USES THEREOF
 2.0%;
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 Score 11;
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Length 63;
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 RESULT 13
US-09-248-796A-25289
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 US-08-700-651-14
 US-08-700-651-14
 US-09-248-796A-25289
 Query Match
Best Local S
Matches 11
 NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 25289
SERGTH: 75
TYPE: PRT
ORGANISM: Candida albicans
 SOFTWARE: PatentIn Ver.
SEQ ID NO 14
LENGTH: 91
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 GENERAL INFORMATION:
 Sequence 25289, Apparent No. 674713
 GENERAL INFORMATION:
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 Patent No.
 Sequence 14,
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 CURRENT APPLICATION NUMBER: US/08/700,651B
CURRENT FILING DATE: 1997-08-14
EARLIER APPLICATION NUMBER: 08/415,751
EARLIER FILING DATE: 1995-04-03
NUMBER OF SEQ ID NOS: 15
 APPLICANT: PETERSEN, CAROLYN
APPLICANT: LEECH, JAMES
APPLICANT: NELSON, RICHARD, C.
APPLICANT: GUT, JIRI
 FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR TILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
 TITLE OF INVENTION: VACCINES, ANTIBODIES, PROTEINS, GLYCOPROTEINS, DNAS AND TITLE OF INVENTION: FOR PROPHYLAXIS AND TREATMENT OF Cryptosporidium parvum TITLE OF INVENTION: INFECTIONS FILE REFERENCE: 480.19-4(HV)
 APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
 TYPE: PRT
ORGANISM: Cryptosporidium parvum
 OTHER INFORMATION: mutant/variant of SEQ ID NO:5
 FEATURE:
 Local Similarity
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 393
 393
 393 TTTTTTTTT 403
 37
18
 7
 .4, Application US/08700651B
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 TTTTTTTTTT 47
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 Application US/09248796A
 2.0%; Score 11; DB 2;
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 RELATING TO CANDIDA ALBICAN
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US-08-328-318-19

Sequence 19, Application US/08928361B

Patent No. 607151B

GEMERAL INFORMATION:
APPLICANT: Peteram, Carclyn
TITLE OF INVENTION: PEPFIDES, POLYREPTIDES, MALOSS AND FRAGMENTS
TITLE OF INVENTION: FREIT EMPCTIONAL MUTANTS, VARIANTS, ANALOSS AND FRAGMENTS
TITLE OF INVENTION: FOR TRAMMENT AND DETECTION/DIAGNOSIS OF CRYPTOSPORIDIUM
TITLE OF INVENTION: SPECIES INFECTIONS
CONTRESSES: PETERS, VERMY, JONES & BIKSA
STREET: 385 Sherman Avenue, Suite 6
STATE: CA
MUTHER PAJOS LAVO
COMPUTER RADABLE FORM:
MEDIUM TIPE: PLOPPY disk
MEDIUM TIPE: PLOPPY disk
MEDIUM TIPE: PLOPPY
COMPUTER READABLE FORM:
MEDIUM TIPE: PLOPPY
COMPUTER REA
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| Sequence 34,                                                                                                                                                                                                              |                                                                                                                                                                                                                                                                                                                                           |                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | ) O O O O O O O O O O O O O O O O O O O                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
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| 607<br>608<br>610<br>611                                                                                   | 604<br>606                                         | 602<br>603                       | 600            | 598<br>8            | 596<br>597 | 155        | 593               | 591<br>592                       | 590  | 589        | 587      | 586 | 7 7<br>2 8<br>4 7 | 583 | 582        | 580<br>581 | 579        | 578           | 576 | 574               | 573      | 571   | 570   | 5 6 6<br>6 6 6 | 567 | 55 O | 564  | 563    | 561        | ກ ທ<br>ດ ທ | 558 | 557          | 3 5 5<br>5 br>5<br>5<br>5<br>5<br>5<br>5<br>5<br>5<br>5<br>5<br>5<br>5<br>5<br>5<br>5<br>5<br>5<br>5 | 554        | 553                   | 551  | 550 | 549   | 547 | 546 | 545                   | ກ ທ<br>4 4<br>4 4          | 542 | 541                | 540                |
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|                                                                                                            | 111                                                | ##                               | ==             | 11                  | 11         | :::        | : ::              | 11                               | : 11 | ##         | : ::     | ۲;  | :                 | ::: | 片          | 11         | <b>;</b> ; | 11            | 11  | 11                | :::      | : 1:  | 11    | : ::           | :1: |      | 11   |        |            | 111        | H   | 11           | 11                                                                                                                                                                                                                                                                                                                                                               | : ::       | 11                    | : :: | 11  | ===   | 11  | ::: | ۲:                    | 11                         | 11  | 11                 | 11                 |
| ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,                                                                     |                                                    |                                  |                |                     |            |            |                   |                                  |      |            |          |     |                   |     |            |            |            |               |     |                   |          |       |       |                |     |      |      |        |            |            |     |              |                                                                                                                                                                                                                                                                                                                                                                  |            |                       |      |     |       |     |     |                       |                            |     |                    |                    |
| 4444<br>444<br>0000                                                                                        | 444                                                | 44                               | 44             | 44                  | 44         |            | 4.4               | 44                               | 4    | 44         | <u>.</u> | 4   | 4                 |     | <u> </u>   | 2 2        | <u> </u>   | 440           |     | 4 4<br>4 4<br>0 0 | <u> </u> | 4 4 0 | 440   | 4 4            |     |      | 440  | ~ ~    | 440        | 440        |     |              | 440                                                                                                                                                                                                                                                                                                                                                              |            | 440                   | 440  | 440 | 440   | 440 | 440 | 440                   | 440                        | -   |                    | 440                |
| 4 US-10-179-521-34<br>4 US-10-202-475-34<br>4 US-10-195-887-34<br>4 US-10-195-893-34<br>4 US-10-179-509-34 | US-10-176-983-<br>US-10-176-988-<br>US-10-179-517- | US-10-176-752-<br>US-10-176-981- | US-10-176-486- | -Sn                 | -SD        | us-        | -su               | US-10-176-984-<br>US-10-179-508- | -Sn  | -SO        | uş-      | us- | - 20              | -Su | US-        | us-        | -S         |               | us- | <br>              | US-      |       |       |                |     |      |      | S. US- | us-        | -Su        | .Sn | S. S.        | Su                                                                                                                                                                                                                                                                                                                                                               | -Sn        | S S                   | .su  | US- | S.O.  | .Sn | S.  |                       |                            | Su  | US-10-184-657      | 0-184-624          |
|                                                                                                            | ωωω<br>4 4 4                                       | ωωι<br>4.4.                      | 3 4 4          | 0 34                | ωω<br>4 4  | υ ι.<br>4. | 34                | 34,                              | 34,  | ω ω<br>4 4 | 34       | 344 | 34,               | 34, | ω μ<br>4.4 | υ<br>4.    | 34,        | 3 4<br>4<br>7 | 34, | ω ω<br>4. 4.      | 34,      | 34,   | 34,   | 34             | 34, | 34.4 | 34,  | 3 4    | 34,        | . ω<br>4.  | 34. | ω (ι<br>42 4 | 3 44                                                                                                                                                                                                                                                                                                                                                             | 34,        | ا<br>ا<br>ا<br>ا<br>ا | 34,  | 34, | 1 U U | עונ | 34, | 10 L<br>13 L<br>14 .4 | 10<br>14<br>14<br>14<br>14 | 34, | ω ι                | י עו               |
|                                                                                                            |                                                    |                                  |                |                     |            |            |                   |                                  |      |            | -        |     |                   |     |            |            |            |               |     |                   |          |       |       |                |     |      |      |        |            |            |     |              |                                                                                                                                                                                                                                                                                                                                                                  |            |                       |      |     | -     |     |     |                       |                            |     |                    | _                  |
| 0 0 0 0 0 0<br>0 0 0 0 0 0<br>0 0 0 0 0 0                                                                  | 678<br>679                                         | 675<br>676                       | 673            | 671                 | 669<br>670 | 668        | 666               | 664<br>665                       | 663  | 661<br>662 | 660      | 659 | 657               | 656 | 55 S       | 653        | 652        | 050           | 649 | 647               | 646      | 644   | 643   | 641            | 640 | 638  | 637  | 635    | 634        | 632        | 631 | 630          | 628                                                                                                                                                                                                                                                                                                                                                              | 627        | 5 S S                 | 624  | 623 | 621   | 620 | 619 | 618                   | 616                        | 615 | 614                | 612                |
| ::::::                                                                                                     | 222                                                | ==:                              | :::            | 12;                 | :::        | 11         | :::               | 11                               | 11   | 11         | 11       | 11  | : ::              | 11  | 11         |            | 11         | ::            | 11  |                   | 11       | :::   | 11 11 | : 1:           | 11  | : 11 | 11   | 11     | <b>:</b> : | 11         | 11  | <b>:</b> ::  | :::                                                                                                                                                                                                                                                                                                                                                              | <b>:</b> ; | : ::                  | 11   | 11  | : ;;  | 11  | 11  |                       | ::                         | 11  | 11 1               | <b>:</b> ;         |
| 00000                                                                                                      |                                                    |                                  |                |                     |            |            |                   |                                  |      |            |          |     |                   |     |            |            |            |               |     |                   |          |       |       |                |     |      |      |        |            |            |     |              |                                                                                                                                                                                                                                                                                                                                                                  |            |                       |      |     |       |     |     |                       |                            |     |                    |                    |
| 694<br>707<br>4<br>5                                                                                       |                                                    |                                  |                |                     |            |            |                   |                                  |      |            |          |     |                   |     |            |            |            |               |     |                   |          |       |       |                |     |      |      |        |            |            |     |              |                                                                                                                                                                                                                                                                                                                                                                  |            |                       |      |     |       |     |     |                       |                            |     | 44                 | 440                |
| US-10-952-045-22<br>US-10-1952-045-22<br>US-10-1952-045-23                                                 |                                                    | Sus                              | មួន            | US-10-425-114-58445 | Su         | S          | US-10-278-536-182 | S S                              | S    | SUS        | S        | ยูย | SD                | SD  | :<br>:0 :: | Sus        | S          | Su            | SS  | S                 | S        | Sn    | S     | ខ្ល            | SD  | Sus  | gs o | SS     | SO         | Sn         | នួន |              | SUS                                                                                                                                                                                                                                                                                                                                                              | នួន        | SUS                   | SD   | SD  | S C   | S   | US  | us<br>Su              | ន                          | ទូន | 4 US-10-198-759-34 | 1 10-10-104-000-24 |
|                                                                                                            |                                                    |                                  |                |                     |            |            |                   |                                  |      |            |          |     |                   |     |            |            |            |               |     |                   |          |       |       |                |     |      |      |        |            |            |     |              |                                                                                                                                                                                                                                                                                                                                                                  |            |                       |      |     |       |     |     |                       |                            |     |                    |                    |

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| US-10-141-/59-243 US-10-140-864-243 US-10-184-644-275 US-10-184-634-275 US-10-184-634-275 US-10-123-155-51 US-10-146-731-51 US-10-140-472-51 US-10-141-761-51 US-10-142-885-51 US-10-143-790-51 US-10-137-871-51 US-10-137-871-51 US-10-137-871-51 US-10-137-871-51                                                  | US-10-146-731-243<br>US-10-146-472-243<br>US-10-141-761-243<br>US-10-142-885-243<br>US-10-158-790-243<br>US-10-158-790-243<br>US-10-10-923-243<br>US-10-141-756-243<br>US-10-141-756-243                                                                                                       | US-10-146-731-155 US-10-140-472-155 US-10-141-761-155 US-10-142-885-155 US-10-138-790-155 US-10-138-790-155 US-10-140-923-155 US-10-141-756-155 US-10-141-759-155 US-10-140-805-155 US-10-140-805-155 US-10-140-805-155 US-10-140-805-155                                                                                                 | US-11-097-143-22779 US-10-073-912-13 US-10-123-155-29 US-10-146-731-29 US-10-141-761-29 US-10-142-885-29 US-10-148-790-29 US-10-137-871-29 US-10-140-923-29 US-10-141-756-29 US-10-141-756-29 US-10-141-756-29 US-10-140-805-29 US-10-140-805-29 US-10-140-805-29 US-10-140-805-29 US-10-140-805-29 US-10-140-805-29 US-10-140-805-29 US-10-140-805-29 US-10-140-805-29                                                                                 | US-11-097-143-32844 US-10-450-763-57590 US-10-450-763-57590 US-10-32-585-7117 US-10-32-923-3091 US-10-184-644-247 US-10-184-634-247 US-10-121-882-2 US-10-121-882-2 US-10-732-923-9614 US-10-732-923-9614 US-10-732-923-9614 US-10-732-923-9614 US-10-732-923-9614 US-10-732-923-13550 US-11-097-143-23112 US-11-097-143-30609 US-11-097-143-30609 US-11-188-298-10688 US-10-282-122A-63575 US-10-282-122A-63575 US-11-097-143-37923 US-11-097-143-37923 US-11-097-143-37923                                                                                                                                                                                                                                                |
|                                                                                                                                                                                                                                                                                                                      | equence 243                                                                                                                                                                                    | 1555<br>1555<br>1555<br>1555<br>1555<br>1555<br>1555                                                                                                                                                                                                                                                                                      |                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 328<br>328<br>328<br>39<br>30<br>31<br>31<br>31<br>31<br>31<br>31<br>31<br>31<br>31<br>31                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
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|                                                                                                                                                                                                                                                                                                                      |                                                                                                                                                                                                                                                                                                | 798<br>801<br>802<br>803<br>804<br>806<br>806                                                                                                                                                                                                                                                                                             | 782<br>783<br>785<br>786<br>786<br>787<br>791<br>791<br>792<br>793<br>795                                                                                                                                                                                                                                                                                                                                                                               | 758<br>759<br>760<br>762<br>763<br>764<br>765<br>766<br>767<br>768<br>769<br>770<br>771<br>771<br>772<br>773<br>773<br>774<br>778<br>778                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
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| 819 11 2.0 2750 4<br>820 11 2.0 2750 4<br>821 11 2.0 2750 4<br>822 11 2.0 2750 4<br>823 11 2.0 2750 4<br>824 11 2.0 2750 4<br>825 11 2.0 2750 4<br>826 11 2.0 2750 4<br>827 11 2.0 2750 4<br>828 11 2.0 2750 4<br>829 11 2.0 2750 4<br>829 11 2.0 2750 4<br>829 11 2.0 2750 4<br>820 11 2.0 2750 4<br>821 2.0 2750 4 | 810 11 2.0 2454 4<br>811 11 2.0 2454 4<br>812 11 2.0 2454 4<br>813 11 2.0 2454 4<br>814 11 2.0 2454 4<br>815 11 2.0 2454 4<br>816 11 2.0 2478 4<br>817 11 2.0 2478 4<br>818 11 2.0 2478 4                                                                                                      | 111 2.0 2197 4 111 2.0 2265 4 111 2.0 2265 4 111 2.0 2266 4 111 2.0 2346 6 111 2.0 2344 4 111 2.0 2454 4 111 2.0 2454 4 111 2.0 2454 4 111 2.0 2454 4 111 2.0 2454 4 111 2.0 2454 4                                                                                                                                                       | 111 2.0 2120 4 111 2.0 2120 4 111 2.0 2120 4 111 2.0 2120 4 111 2.0 2128 4 111 2.0 2128 4 111 2.0 2197 4 111 2.0 2197 4 111 2.0 2197 4 111 2.0 2197 4 111 2.0 2197 4 111 2.0 2197 4 111 2.0 2197 4 111 2.0 2197 4 111 2.0 2197 4 111 2.0 2197 4 111 2.0 2197 4 111 2.0 2197 4 111 2.0 2197 4 111 2.0 2197 4 111 2.0 2197 4                                                                                                                              | 11 2.0 2014 4 11 2.0 2014 4 11 2.0 2014 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4 11 2.0 2027 4                                                                       |
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| 896<br>897<br>898<br>899<br>900<br>901<br>902                                                                                                                                        |                                                                                              | w w u                                                                |                          | 88                | ш ш                            | ш ш                             | , 60                           |                                  |                             |                                    |                                    |                                |                                              | 868<br>868                                   |                                |                                                                      |                                                                      |                                              |                                  |                                  |                                                                      |                                  |                                  |                                |                                                                    |                                 |                                  |                                  |                                  |                              |                              |                                   |         |                      |                                              |                      |
|--------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------|----------------------------------------------------------------------|--------------------------|-------------------|--------------------------------|---------------------------------|--------------------------------|----------------------------------|-----------------------------|------------------------------------|------------------------------------|--------------------------------|----------------------------------------------|----------------------------------------------|--------------------------------|----------------------------------------------------------------------|----------------------------------------------------------------------|----------------------------------------------|----------------------------------|----------------------------------|----------------------------------------------------------------------|----------------------------------|----------------------------------|--------------------------------|--------------------------------------------------------------------|---------------------------------|----------------------------------|----------------------------------|----------------------------------|------------------------------|------------------------------|-----------------------------------|---------|----------------------|----------------------------------------------|----------------------|
|                                                                                                                                                                                      | T                                                                                            | 111                                                                  | 22                       | ==                | 11                             | 11                              | :=:                            | ::                               | 11                          | :::                                | 11                                 | ==                             | ==                                           | :::                                          | ===                            | ::::                                                                 | ===                                                                  | :::                                          | :1:                              | 11                               | 11 1                                                                 | 11                               | 11                               | 11                             | :::                                                                | 11                              | :::                              | ::                               | :::                              | 11                           | 11                           | 11                                | :::     | 11                   | 11                                           | :::                  |
| NNNNNNNN<br>0000000                                                                                                                                                                  |                                                                                              |                                                                      |                          |                   |                                |                                 |                                |                                  |                             |                                    |                                    |                                |                                              |                                              |                                |                                                                      |                                                                      |                                              |                                  |                                  |                                                                      |                                  |                                  |                                |                                                                    |                                 |                                  |                                  |                                  |                              |                              |                                   |         |                      |                                              | 2.0                  |
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| 4 US-10-137-871-197<br>4 US-10-140-923-197<br>4 US-10-141-756-197<br>4 US-10-141-759-197<br>4 US-10-140-805-197<br>4 US-10-140-864-197<br>4 US-10-140-864-351<br>4 US-10-184-634-351 | 22 22 23<br>22 23 23                                                                         | 222                                                                  | US US                    | SUS               | នួន                            | ខ្លួ                            | 56.5                           | . US                             | 88                          | 5 5 5                              | 5 E                                | ខ្លួន                          | g g                                          | ផ្លួ                                         | ធ្លូច្ច                        | 566                                                                  | 5 5                                                                  | , g, g                                       | : F. S                           | 3 5                              | ផ្លួ                                                                 | ı g                              | 3 5                              | ۶, F                           | ផ្ល                                                                | <u> </u>                        | g                                | <u> </u>                         | g                                | ទ្ធ ខ្ល                      | g                            | g g                               | 5 5     | ₫ 55                 | 5 5                                          | g                    |
| Sequence 197, App<br>Sequence 197, App<br>Sequence 197, App<br>Sequence 197, App<br>Sequence 197, App<br>Sequence 197, App<br>Sequence 351, App<br>Sequence 351, App                 | 197<br>197<br>197<br>197                                                                     | 14,<br>197                                                           | 537                      | 537               | 537                            | 537                             | 537                            | 537                              | 411<br>537                  | 411                                | 3,5                                | 3,35                           | ູ<br>ພູບ<br>ພູບ                              | 35,                                          | 35,                            | 35,                                                                  | 77,                                                                  | 261                                          | 51,                              | 285                              | 285                                                                  | 285                              | 285                              | 285                            | 285                                                                | 285                             | 285                              | 229                              | 229                              | 229                          | 229                          | 229                               | 229     | 229                  | 225                                          | 307                  |
|                                                                                                                                                                                      |                                                                                              |                                                                      |                          |                   |                                |                                 |                                |                                  |                             |                                    |                                    |                                |                                              |                                              |                                |                                                                      |                                                                      |                                              |                                  |                                  |                                                                      |                                  |                                  |                                |                                                                    |                                 |                                  |                                  |                                  |                              |                              |                                   |         |                      |                                              |                      |
| 969<br>970<br>971<br>973<br>974<br>975                                                                                                                                               | 965<br>967<br>968                                                                            | 962<br>963                                                           | 960<br>961               | 958               | 956                            | 954                             | 953                            | 951                              | 949                         | 948                                | 946                                | 944                            | 942<br>943                                   | 940<br>941                                   | 938<br>939                     | w w                                                                  | ww                                                                   | 932<br>933                                   | $\omega$                         |                                  | $\sim$                                                               | $\sim$ $\sim$                    | $\sim$                           | $\sim$                         | $\sim$ $\sim$                                                      | <i>,</i> –                      |                                  |                                  | $\rightarrow$                    |                              | -                            |                                   | 00      | າດ                   | 906                                          | 0                    |
| 969<br>970<br>10<br>971<br>10<br>972<br>10<br>973<br>10<br>974<br>10<br>975<br>10                                                                                                    | 111111                                                                                       | 2 2 2                                                                | 100                      |                   | 7 6 0                          | 4. 7.                           | 33 2                           | , p. 3                           | 50 9                        | 18                                 | 3 6 6                              | 14.7                           | <del>ω</del> δ                               | 76                                           | 36                             | 376                                                                  | 35                                                                   | 332                                          | 31                               | 29                               | 27                                                                   | 26                               | 24.                              | 23                             | 21                                                                 |                                 | 18                               | 16                               | 15                               | 13                           | 12                           |                                   | 09      | 07                   | 06 5                                         | 04                   |
|                                                                                                                                                                                      | 10 1.<br>7 10 1.<br>10 1.                                                                    | 10 1.                                                                | 10 1.                    | 1001              | 56 10 1.<br>57 10 1.           | 10 1.                           | 10 1.                          | 100                              | 10 1.                       | 18 10 1.                           | 10 1.                              | 10 1.                          | 12 10 1.<br>13 10 1.                         | 10 10 1.                                     | 38 10 1.<br>39 10 1.           | 36 10 1.<br>37 10 1.                                                 | 34 10 1.<br>35 10 1.                                                 | 32 10 1.<br>33 10 1.                         | 10 1.                            | 29 10 1                          | 27 10 1.<br>28 10 1.                                                 | 26 10 1                          | 24 10 1                          | 22 10 1<br>23 10 1             | 21 10 1.                                                           | 19 10 1                         | 18 10 1                          | 16 10 1                          | 15 10 1                          | 13 10 1                      | 12 10 1                      | 10 11 2                           | 09 11 2 | 07 11 2              | 05 11 2<br>06 11 2                           | 04 11 2              |
| 10 1.8 535<br>10 10 1.8 579<br>10 1.8 625<br>10 1.8 648<br>10 1.8 788<br>10 1.8 788                                                                                                  | 10 1.8 535<br>10 1.8 535<br>10 1.8 535<br>10 1.8 535                                         | 52 10 1.8 535<br>53 10 1.8 535<br>54 10 1.8 535                      | 10 1.8 535<br>10 1.8 535 | 10 1.8 535        | 56 10 1.8 528<br>57 10 1.8 528 | 54 10 1.8 491<br>55 10 1.8 525  | 53 10 1.8 471<br>53 10 1.8 489 | 10 1.8 412                       | 19 10 1.8 335<br>10 1.8 335 | 18 10 1.8 335                      | 10 1.8 335                         | 14 10 1.8 316<br>15 10 1 8 325 | 12 10 1.8 265<br>13 10 1.8 307               | 10 1.8 256<br>11 10 1.8 259                  | 38 10 1.8 254<br>39 10 1.8 255 | 36 10 1.8 253<br>37 10 1.8 253                                       | 34 10 1.8 244<br>35 10 1.8 253                                       | 32 10 1.8 222<br>33 10 1.8 224               | 31 10 1.8 222                    | 29 10 1.8 195                    | 27 10 1.8 158<br>28 10 1.8 171                                       | 26 10 1.8 151                    | 24 10 1.8 125                    | 22 10 1.8 103<br>23 10 1.8 115 | 21 10 1.8 101                                                      | 19 10 1.8 10                    | 1/ 10 1.8 10<br>18 10 1.8 10     | 16 10 1.8 10                     | 15 10 1.8 10                     | 13 10 1.8 10<br>14 10 1.8 10 | 12 10 1.8 10<br>12 10 1.8 10 | 10 11 2.0 35823                   | 08      | 07 11 2.0 4640       | 05 11 2.0 4563<br>06 11 2.0 4640             | 04 11 2.0 4563       |
|                                                                                                                                                                                      | 55 10 1.8 535 4 US-1<br>66 10 1.8 535 4 US-1<br>77 10 1.8 535 4 US-1<br>18 10 1.8 535 4 US-1 | 32 10 1.8 535 4 US-1<br>33 10 1.8 535 4 US-1<br>34 10 1.8 535 4 US-1 | 50 10 1.8 535 4 US-1     | 10 1.8 535 4 US-1 | 56 10 1.8 528 4 US-1           | 10 1.8 491 4 US-10-032-585-7161 | 53 10 1.8 471 4 US-1           | 10 1.8 412 4 US-10-424-599-16522 | 10 1.8 335 4 US-1           | 18 10 1.8 335 4 US-10-3/4-780A-206 | 16 10 1.8 335 4 US-10-225-066A-222 | 10 1.8 316 6 US-11-087-099-759 | 12 10 1.8 265 4 US-1<br>13 10 1.8 307 6 US-1 | 10 10 1.8 256 4 US-1<br>11 10 1.8 259 6 US-1 | 38                             | 36 10 1.8 253 4 US-10-412-699B-1<br>37 10 1.8 253 5 US-10-732-923-54 | 34 10 1.8 244 4 US-10-424-599-17<br>35 10 1.8 253 4 US-10-278-173-44 | 32 10 1.8 222 6 US-1<br>33 10 1.8 224 5 US-1 | 30 10 1.8 213 4 US-10-424-599-28 | 29 10 1.8 195 6 US-11-097-143-34 | 27 10 1.8 158 4 US-10-425-114-50<br>28 10 1.8 171 4 US-10-437-963-20 | 26 10 1.8 151 4 US-10-424-599-19 | 24 10 1.8 125 4 US-10-425-115-20 | 22                             | 20 10 1.8 11 6 US-11-103-356A-<br>21 10 1.8 101 4 US-10-424-599-19 | 19 10 1.8 10 6 US-11-103-356A-4 | 1/ 10 1.8 10 3 US-09-573-822C-56 | 16 10 1.8 10 3 US-09-573-822C-55 | 15 10 1.8 10 3 US-09-573-822C-55 | 13 10 1.8 10 3 US-0          | 12                           | 10 11 2.0 35823 5 US-10-874-049-1 | 08      | 07 11 2.0 4640 4 US- | 05 11 2.0 4563 4 US-<br>06 11 2.0 4640 4 US- | 04 11 2.0 4563 4 US- |

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RESULT 1
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US-11-134-563-12
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 APPLICANT: Leong, John M.

APPLICANT: Leong, John M.

APPLICANT: Campellone, Kenneth G.

TITLE OF INVENTION: ESPFU NUCLEIC ACIDS AND

TITLE OF INVENTION: USES THEREOF

FILE REFERENCE: 07917-280001

CURRENT APPLICATION NUMBER: US/11/134,563

CURRENT FILING DATE: 2005-05-20

PRIOR APPLICATION NUMBER: US 60/573,600

PRIOR APPLICATION NUMBER: US 60/573,600
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TITLE OF INVENTION: CONTROL OF THERAPEUTIC TITLE OF INVENTION: PROTEINS OF THERAPEUTIC FILE REFERENCE: 30853/40359A

CURRENT FILING DATE: 2005-02-07

CURRENT FILING DATE: 2005-02-07

PRIOR APPLICATION NUMBER: US 60/589,227

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

PRIOR FILING DATE: 2004-07-20

PRIOR APPLICATION NUMBER: IN 173/DEL/2004

PRIOR APPLICATION NUMBER: National Substitution of Section 3.3

SOFTWARE: PatentIn version 3.3

SEQ ID NO 20

LENGTH: 558

TYPE: PRT

ORGANISM: Escherichia coli 0157:H7
 RESULT 2
US-11-052-554A-20
 US-11-052-554A-20
 Sequence 20, Application US/11052554A Philication No. US20050288866A1 GENERAL INFORMATION:
APPLICANT: Sachdeva, et al.
 Matches
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 TITLE OF INVENTION: COMPUTATIONAL METHOD FOR TITLE OF INVENTION: PROTEINS OF THERAPEUTIC
 Local Similarity
 301
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TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement: PILE REFERENCE: 38-21(5323)B: CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 207017
LENGTH: 107
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 US-10-424-599-207017
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 US-10-470-048B-73
 RESULT 3
 US-10-470-048B-73
 Sequence 73, Application US/10470048B
Publication No. US20050037444A1
GENERAL INFORMATION:
APPLICANT: MEINKE ET AL.
TITLE OF INVENTION: A METHOD FOR IDENTIFICATION, ISOLATIÓN AND PRODUCTION
TITLE OF INVENTION: ANTIGENS TO A SPECIFIC PATHOGEN
FILE REFERENCE: SONN:035US
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT APPLICATION NUMBER: US/10/470,048B
CURRENT FILING DATE: 2003-07-25
NUMBER OF SEQ ID NOS: 603
SOFTWARE: Patentin version 3.1
SEQ ID NO 736
 GENERAL INFORMATION:
 Sequence 207017, Application US/10424599 Publication No. US20040031072A1
 Matches
 Best Local Similarity
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OTHER INFORMATION: Clone ID: PAT_MRT3847_28963C.1.pep 10-424-599-207017
 FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(107)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
 LENGTH: 166
TYPE: PRT
ORGANISM: Staphylococcus aureus
 ORGANISM: Glycine max
 ENGTH: 107
 541
 392 QITTTTTTTTTT 404
 541 SAVNTSNNPPAPGSHRFV 558
 481
 481 NMGNTDSVVYSTIQHPPRDTTDNGARLLGNPSAGIQSTYARLALSGGLRHDMGGLTGGSN 540
 421
 421
 361
 43
 QTTTTTTTTTTS 55
 SAVNTSNNPPAPGSHRFV 558
 NVDTPGSEDTMESRRSSMASTSSTFFDTSSIGTVQNPYADVKTSLHDSQVPTSNSNTSVQ 480
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 AGYGLSGALILGGGIGVAVTAALHRKNOPVEQTTTTTTTTTTTSARTVENKPANNTPAQG
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 2.3%; Score 13; DB 5; 100.0%; Pred. No. 0.0031;
 0
 Mismatches
 Length 166;
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SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 1796
LENGTH: 361
TYPE: PRT
ORGANISM: Homo sapiens
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 US-10-017-161-1796
 RESULT 6
 US-10-425-115-366802
 US-10-425-115-366802
 GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
 TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants FILE REFERENCE: 38-21(53222)B CURRENT APPLICATION NUMBER: US/10/425,115 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 369326 SEQ ID NO 366802 LENGTH: 278
 Sequence 1796, Application US/10017161 Publication No. US20030143668A1 GENERAL INFORMATION:
 Query Match
Best Local (
 Matches
 Sequence 366802, Application US/10425115 Publication No. US20040214272A1
 APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: AKIYAWA, YUTAKA
APPLICANT: AKUYAWA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 084335/0152
CURRENT APPLICATION NUMBER: US/10/017,161
CURRENT FILING DATE: 2002-12-18
 Query Match
 Matches
 Best
 Query Match
 PRIOR APPLICATION NUMBER: JP 2001/246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2430
 FEATURE: OTHER INFORMATION: Clone ID: MRT4577_9768C.1.pep
 TYPE: PRT
ORGANISM: Zea mays
 Local Similarity hes 12; Conserv
 Local Similarity
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 393 TTTTTTTTTTS 404
 392 QTTTTTTTTTT 403
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 TTTTTTTTTTS 404
 TTTTTTTTTTS 32
TTTTTTTTTTS 345
 QTTTTTTTTTT 63
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 2.2%; Score 12; DB
100.0%; Pred. No. 0.0
tive 0; Mismatches
 2.2%; Score 12; DB 4; 00.0%; Pred. No. 0.053;
 Score 12;
; Pred. No.
 Mismatches
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 DB 4; Length 278; 0.042;
 DB 4; Length 107; 0.018;
 Length 361;
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 Indels
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PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
PRIOR FILING DATE: 2001-06-18
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1452
LENGTH: 361
; Sequence 30426, Application US/11097143
; Publication No. US20050208558A1
; GENERAL INFORMATION:
; APPLICANT: Venter, J. Craig
; APPLICANT: et al.
 RESULT 8
US-10-424-599-144079
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 RESULT 9
US-11-097-143-30426
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 ; ORGANISM: Homo sapiens US-10-292-798-1452
 US-10-292-798-1452
 US-10-424-599-144079
 Sequence 144079, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Chou Yihua
APPLICANT: Chou Yihua
APPLICANT: Co Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 144079
LENGTH: 367
TYPE: PRT
 Sequence 1452, Application US/10292798 Publication No. US20030235833A1 GENERAL INFORMATION:
 Query Match
Best Local Similarity
 Matches
 Matches 12;
 Query Match
 FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
 APPLICANT: AKIYAMA, YUTAKA
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
 APPLICANT: SUWA, MAKIKO APPLICANT: ASAI, KIYOSHI
 OTHER INFORMATION: Clone ID: PAT_MRT3847_101115C.1.pep
 ORGANISM: Glycine max FEATURE:
 2.2%;
Local Similarity 100.0%;
ses 12; Conservative 0
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 241 Tritrititis 252
 393 TITTTTTTTTS 404
 TTTTTTTTTTS 345
 Conservative
 100.0%;
 2.2%; Score 12; DB 4; Length 367; 00.0%; Pred. No. 0.054;
 Score 12; DB 4; Length 361; Pred. No. 0.053;
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 0; Mismatches
 Mismatches
 0; Indels
 <u>,</u>
 0
 Gaps
 0
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 FILE REFERENCE: CLOOO728

CURRENT APPLICATION NUMBER: US/11/097,143

CURRENT FILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: 60/157,832

PRIOR FILING DATE: 1999-10-05

PRIOR FILING DATE: 1999-10-19

PRIOR PRIOR APPLICATION NUMBER: 60/161,932

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR PRILING DATE: 1999-10-28

PRIOR PRILING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR FILING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: 60/173,383

PRIOR FILING DATE: 1999-12-28

PRIOR APPLICATION NUMBER: 60/175,693

PRIOR FILING DATE: 2000-01-12

PRIOR APPLICATION NUMBER: 60/184,831

PRIOR APPLICATION NUMBER: 60/184,831

PRIOR APPLICATION NUMBER: 60/184,831

PRIOR APPLICATION NUMBER: 60/191,637

PRIOR APPLICATION NUMBER: 60/191,637

PRIOR PILING DATE: 2000-03-23

PRIOR FILING DATE: 2000-03-23

PRIOR FILING DATE: 2000-03-23

PRIOR FILING DATE: 2000-03-23
밁
 ; TYPE: PRT ; ORGANISM: Candida albicans US-10-741-849-7161
 RESULT 10
US-10-741-849-7161
 US-11-097-143-30426
 TITLE OF INVENTION: Nucleic Acids Encoding Anti-fungal Drug Targets
TITLE OF INVENTION: Use
FILE REFERENCE: 10182-023-999
CURRENT APPLICATION NUMBER: US/10/741,849
CURRENT FILING DATE: 2003-12-19
PRIOR APPLICATION NUMBER: US 60/434,832
PRIOR FILING DATE: 2002-12-19
PRIOR FILING DATE: 2002-13-19
NUMBER: OF SEQ ID NOS: 8000
SOFTWARE: Patentin version 3.2
SEQ ID NO 7161
LENGTH: 785
 NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 30426
LENGTH: 561
 GENERAL INFORMATION:
 Sequence 7161, Application US/10741849 Publication No. US20050019931A1
 Matches
 Query Match
Best Local :
 Matches
 Query Match
Best Local Similarity
 APPLICANT: Roemer, Terry APPLICANT: Jiang, Bo
 APPLICANT: Boone, Charles APPLICANT: Bussey, Howard
 TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE
TITLE OF INVENTION: DROSOPHILA GENES.
 ORGANISM:
 Local Similarity
les 12; Conser
 393
 393 TTTTTTTTTTS 404
 112 TTTTTTTTTTTS 123
16
 12;
TTTTTTTTTTS 27
 TTTTTTTTTTS 404
 DROSOPHILA
 2.2%; Score 12; DB 6; Length 561; ilarity 100.0%; Pred. No. 0.079; Conservative 0; Mismatches 0; Indels
 Conservative
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100.0%; Pred. No.
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 Gaps
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 and Methods
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RESULT 11

US-11-188-298-5674

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RESULT 13
US-10-363-946-2
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 US-11-188-298-20820
 RESULT 12
US-11-188-298-20820
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 US-11-188-298-5674
 Sequence 2, Application US/10363946 Publication No. US20050037436A1 GENERAL INFORMATION:
 SEQ ID NO 20820
LENGTH: 802
TYPE: PRT
 APPLICANT: Abad, Mark S. et al.
TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21(53452)B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR FILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22369
SEQ ID NO 5674
 Sequence 20820, Application US/11188298 Publication No. US20060075522A1 GENERAL INFORMATION:
 Matches
 Query Match
 Sequence 5674, Application US/11188298 Publication No. US20060075522A1 GENERAL INFORMATION:
 Matches
 Query Match
 APPLICANT: Abad, Mark S. et al.

TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-21 (53452) B
CURRENT APPLICATION NUMBER: US/11/188,298
CURRENT FILING DATE: 2005-07-22
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR APPLICATION NUMBER: 60/592,978
PRIOR FILING DATE: 2004-07-31
NUMBER OF SEQ ID NOS: 22569
 APPLICANT: Saeger, Beate
TITLE OF INVENTION: Test Systems and the Use Thereof for Identifying and
TITLE OF INVENTION: Characterizing Compounds
FILE REFERENCE: LeA 34 240
CURRENT APPLICATION NUMBER: US/10/363,946
CURRENT FILING DATE: 2003-03-07
 APPLICANT: von Samson-Himmelstjerna, Georg
APPLICANT: Harder, Achim
APPLICANT: Wunderlich, Frank
 APPLICANT:
 APPLICANT: Bayer Aktiengesellschaft
 ORGANISM: Ruminococcus flavefaciens
 LENGTH: 802
TYPE: PRT
 ORGANISM: Ruminococcus flavefaciens
 Local Similarity
 Local Similarity
 533
 393
 393 TTTTTTTTTTTS 404
 533 Tritritiris 544
 12;
 TTTTTTTTTTS 544
 Schmitt-Wrede, Hans-Peter
 2.2%; Score 12; DB 6; ilarity 100.0%; Pred. No. 0.11; Conservative 0; Mismatches
 2.2%; Score 12; DB ilarity 100.0%; Pred. No. 0. Conservative 0; Mismatches
 | TITTTTS 404
TE: 2003-03-07
NUMBER: PCT/EP01/09771
: 2001-08-24
 DB 6;
 0
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 Length 802;
 Length 802;
 Indels
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 Gaps
 Gaps
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 片
 US-11-097-143-19809
 APPLICANT: Venter, J. Craig
APPLICANT: Venter, J. Craig
APPLICANT: Venter, J. Craig
APPLICANT: Venter, J. Craig
TITLE OF INVENTION: DETECTION KIT, SUCH AS NU
TITLE OF INVENTION: DROSOPHILA GENES.
FILE REFERENCE: CLO00728
CURRENT APPLICATION NUMBER: US/11/097,143
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR APPLICATION NUMBER: 60/157,832
PRIOR FILING DATE: 1999-10-05
 S
 US-11-097-143-19809
 US-10-363-946-2
 NUMBER OF SEQ ID NOS: 43008
SOFTWARE: FRETSEQ for Windows Version
SEQ ID NO 19809
LENGTH: 1026
 Query Match 2.2%; S
Best Local Similarity, 100.0%;
Matches 12; Conservative 0;
 GENERAL INFORMATION:
 Sequence 19809, Application US/11097143
Publication No. US20050208558A1
 SEQ ID NO 2
 Matches 12;
 Query Match
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 PRIOR APPLICATION NUMBER: 60/175,693
PRIOR FILING DATE: 2000-01-12
PRIOR APPLICATION NUMBER: 60/184,831
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: 60/191,637
PRIOR FILING DATE: 2000-03-23
 PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: DE100 53 785.5
PRIOR FILING DATE: 2000-10-30
 PRIOR APPLICATION NUMBER: 60/164,769
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/173,383
PRIOR FILING DATE: 1999-12-28
 PRIOR FILING DATE: 1999-10-19
PRIOR APPLICATION NUMBER: 60/161,932
PRIOR FILING DATE: 1999-10-28
 NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.2
 PRIOR APPLICATION NUMBER: 60/160,191
 PRIOR APPLICATION NUMBER: DE100 44 098.3
 ORGANISM:
 TYPE: PRT ORGANISM: Haemonchus contortus
 TYPE: PRT
 LENGTH: 986
 509
 393
 133 TTTTTTTTTTS 144
 393 TTTTTTTTTTS 404
 Similarity
TTTTTTTTTTS 616
 TTTTTTTTTTS 404
 DROSOPHILA
 Conservative
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 DB 5;
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 Length 1026;
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 Indels
 Indels
 OF 10,000 OR MORE
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 Gaps
 Gaps
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RESULT 15 US-11-097-143-38604

Sequence 38604, Application US/11097143 Publication No. US20050208558A1 GENERAL INFORMATION:

Venter, J. Craig

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APPLICANT: et al.

TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID

TITLE OF INVENTION: DETECTING EXPRESSION OF 10,000 OR MORE

TITLE OF INVENTION: DESOSOPHILA GENES.

FILE REFERENCE: CLORO728

CURRENT APPLICATION NUMBER: US/11/97,143

CURRENT FILING DATE: 1999-10-95

PRIOR APPLICATION NUMBER: 60/161,932

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR APPLICATION NUMBER: 60/164,769

PRIOR APPLICATION NUMBER: 60/175,632

PRIOR APPLICATION NUMBER: 60/175,632

PRIOR APPLICATION NUMBER: 60/175,633

PRIOR APPLICATION NUMBER: 60/175,633

PRIOR APPLICATION NUMBER: 60/175,633

PRIOR PILING DATE: 1999-11-12

PRIOR APPLICATION NUMBER: 60/175,633

PRIOR PILING DATE: 2000-01-23

PRIOR PILING DATE: 2000-01-23

PRIOR PILING DATE: 2000-01-23

INMERS: FastSQ for Windows Version 4.0

SEQ ID NO 38604

LENGTH: 1026

JENGTH: 1026

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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-11-097-143-38604

Ourly Matches 12; Conservative 0; Mismatches 0; Gaps 0;

Search completed: August 1, 2006, 22:53:43

Job time: 195 secs
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US-11-063-439-64
US-11-063-439-24
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e 189, App e 177, App e 179, App e 272, App e 2736, App e 272, App e 272, App e 2736, App e 272, App e 273, App e 272, App e 273, Ap
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| 167<br>168<br>169<br>170                                                                                       | 164                                                               | 162<br>163                                 | 161                                | 59                  | 90 -7                                      | 0, 0                |                     |                     |                                    | _                   |                                            | 7                   | ט ה                 | n Æ                 | 5                   | ; <u>;</u>          |                     |                     |                                    | () H3                                      | 33                  | 3 =                                | 0 0                      | 80              | 26                         | 25              | 23              | 22              |                 | ഗത                         | 7               | יטי              | سا ۵            | ν'n             | - 0                        | .09             | 107                        | 106             | 104<br>105                 | 103               | 2 2                                | 0 4                                    |
|----------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------|--------------------------------------------|------------------------------------|---------------------|--------------------------------------------|---------------------|---------------------|---------------------|------------------------------------|---------------------|--------------------------------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|---------------------|------------------------------------|--------------------------------------------|---------------------|------------------------------------|--------------------------|-----------------|----------------------------|-----------------|-----------------|-----------------|-----------------|----------------------------|-----------------|------------------|-----------------|-----------------|----------------------------|-----------------|----------------------------|-----------------|----------------------------|-------------------|------------------------------------|----------------------------------------|
|                                                                                                                | 122                                                               | 11                                         | 11                                 | :1:                 | 11                                         | 11                  | : ::                | 11                  | 11                                 | 11                  | 111                                        | 11                  | 11                  | : 1                 | 11                  | 11                  | ==                  | :::                 | 11                                 | 11                                         | 11                  | 11                                 | 11                       | 11              | 11                         | 11              | ::              | 11              | 11              | 11                         | 11              | 11               | 11              | :::             | ===                        | ä               | 1<br>1<br>1                | 11              | 11                         | : 1               | 11<br>11                           | 11                                     |
| ,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,                                                                         |                                                                   |                                            |                                    |                     |                                            |                     |                     |                     |                                    |                     |                                            |                     |                     |                     |                     |                     |                     |                     |                                    |                                            |                     |                                    |                          |                 |                            |                 |                 |                 |                 |                            |                 |                  |                 |                 |                            |                 |                            |                 |                            |                   |                                    |                                        |
| 3499<br>3499<br>3700                                                                                           | 498                                                               | 498<br>498                                 | 496                                | 496                 | 496                                        | 496                 | 495                 | 495                 | 494                                | 494                 | 493                                        | 493                 | 491                 | 491                 | 490                 | 490                 | 489                 | 488                 | 488<br>488                         | 488                                        | 486                 | 486                                | 481                      | 479             | 478                        | 476             | 475             | 475             | 472             | 467<br>471                 | 467             | 9 9 9            | 165             | 462             | 461                        | 457             | 397<br>445                 | 317             | 270                        | 131               | 576<br>762                         | 539                                    |
| 7 US-11-063-439-96<br>7 US-11-063-439-222<br>7 US-11-063-439-226<br>7 US-11-063-439-110<br>7 US-11-063-439-110 | US-11-063-439-<br>US-11-063-439-<br>US-11-063-439-                | US-11-063-439-                             | US-11-063-439-                     | US-11-063-439-      | US-11-063-439-                             | US-11-063-439-      | US-11-063-439-      | US-11-063-439-      | US-11-063-439-                     | US-11-063-439-      | US-11-063-439-                             | US-11-063-439-      | US-11-063-439-      | US-11-063-439-      | US-11-063-439-      | US-11-063-439-      | US-11-063-439-      | US-11-063-439-      | US-11-063-439-                     | US-11-063-439-1                            | US-11-063-439-      | US-11-063-439-                     | US-11-063-439-           | US-11-063-439-  | US-11-063-439-             | US-11-063-439-2 | US-11-063-439-  | US-11-063-439-6 | US-11-063-439-  | US-11-063-439-1            | US-11-063-439-  | US-11-063-439-   | US-11-063-439-8 | US-11-063-439-2 | US-11-063-439-1            | US-11-063-439-1 | US-11-063-439-2            | US-11-063-439-1 | US-11-063-439-6            | US-11-063-439-108 | US-11-063-439-2<br>US-11-174-307B- | US-11-063                              |
| Sequence 96, Appl<br>Sequence 222, App<br>Sequence 246, App<br>Sequence 110, App<br>Sequence 110, App          | 2 10 10 11<br>10 10 10 11                                         | <del></del> γ <sub>2</sub>                 | 12 12                              | יטי<br>יים          | , (b                                       | 10 ti               | ין.<br>עוי          | H 6                 | ) N                                | 1                   | เบ<br>เบ                                   | <u>, u</u>          | 20 1                | دار<br>سر ر         | 201                 | , (v                | 2                   | אנ                  | 0 U                                | <u> </u>                                   | N 1                 | ) H                                | H H                      | 101             | - N                        | 20              | אנ              | N 6             | , N             | N 12                       | 71              | ٠.<br>ب ب        | 00 N            | אנ              | 2                          | <u></u>         | ΝŅ                         | equence 1       | equence 6                  | nce 1             | equence 2:                         | Sequence 43, Appl<br>Sequence 62, Appl |
|                                                                                                                |                                                                   |                                            |                                    |                     |                                            |                     |                     |                     |                                    |                     |                                            |                     |                     |                     |                     |                     |                     |                     |                                    |                                            |                     |                                    |                          |                 |                            |                 |                 |                 |                 |                            |                 |                  |                 |                 |                            |                 |                            |                 |                            |                   |                                    |                                        |
| 244<br>244<br>244<br>244<br>244                                                                                |                                                                   |                                            |                                    |                     |                                            |                     |                     | _                   |                                    |                     |                                            |                     |                     | _                   |                     |                     |                     |                     | _                                  |                                            |                     |                                    |                          | 201             | 199<br>200                 | 198             | 196             | 194             | 193             | 191<br>192                 | 190             | 188              | 187             | 185             | 183<br>184                 | 182             | 181                        | 179             | 178                        | 176               |                                    |                                        |
| 240 11<br>241 11<br>242 11<br>243 11<br>244 11                                                                 | 238                                                               | 235 1<br>236 1                             | 234 1                              | 232                 | 230 I<br>231 I                             | 229 1               | 227 1               | 226 1               | 224 1                              | 223 1               | 221 1                                      | 220 1               | 216 1               | 217                 | 216                 | 214                 | 213                 | 211                 | 209                                | 207                                        |                     |                                    |                          | 201 11          | 199 11<br>200 11           | 198 11          | 196 11          | 194 11          | 193 11          | 191 11<br>192 11           | 190 11          | 188 11<br>189 11 | 186 11          | 185 11          | 183 11<br>184 11           | 182 11          | 180 11<br>181 11           | 179 11          | 178 11                     | 176 11            |                                    |                                        |
|                                                                                                                | 237 11 2<br>238 11 2<br>239 11 2                                  | 235 11 2<br>236 11 2                       | 233 11 2                           | 232 11 2            | 230 11 2<br>231 11 2                       | 229 11 2            | 227 11 2            | 226 11 2            | 224 11 2                           | 223 11 2            | 221 11 2                                   | 220 11 2            | 219 11 2            | 217 11 2            | 216 11 2            | 214 11 2            | 212 11 2            | 211 11 2            | 209 11 2                           | 207 11 2<br>208 11 2                       | 206 11 2.           | 204 11 2.<br>205 11 2.             | 202 11 2                 | 111             | 11<br>2.                   | 11 2            | 111 2.          | 11 2            | 111 2           | 11<br>21<br>2              | 111 2           | 111 2            | 11 2            | 111             | 11 2.                      | 11 2.           | 11 2.                      | 11 2.           | 11 2.                      | 11 2.             | 174 11 2.<br>175 11 2.             | 172 11 2                               |
| 11 2.0 3528<br>11 2.0 3529<br>11 2.0 3529<br>11 2.0 3529<br>11 2.0 3529                                        | 237 11 2.0 3528<br>238 11 2.0 3528<br>239 11 2.0 3528             | 235 11 2.0 3526<br>236 11 2.0 3526         | 234 11 2.0 3525<br>234 11 2.0 3525 | 232 11 2.0 3524     | 230 11 2.0 3524<br>231 11 2.0 3524         | 229 11 2.0 3523     | 227 11 2.0 3522     | 226 11 2.0 3521     | 224 11 2.0 3520<br>225 11 2.0 3520 | 223 11 2.0 3520     | 221 11 2.0 3519<br>222 11 2.0 3519         | 220 11 2.0 3519     | 219 11 2.0 3519     | 217 11 2.0 3518     | 216 11 2.0 3518     | 214 11 2.0 3514     | 212 11 2.0 3513     | 211 11 2.0 3512     | 209 11 2.0 3512<br>210 11 2.0 3512 | 207 11 2.0 3512<br>208 11 2.0 3512         | 206 11 2.0 3512     | 204 11 2.0 3511<br>205 11 2.0 3511 | 202 11 2.0 3511 2.0 3511 | 11 2.0 3511     | 11 2.0 3510<br>11 2.0 3511 | 11 2.0 3510     | 11 2.0 3509     | 11 2.0 3508     | 11 2.0 3508     | 11 2.0 3507<br>11 2.0 3508 | 11 2.0 3507     | 11 2.0 3507      | 11 2.0 3507     | 11 2.0 3506     | 11 2.0 3505<br>11 2.0 3506 | 11 2.0 3504     | 11 2.0 3504<br>11 2.0 3504 | 11 2.0 3503     | 11 2.0 3503<br>11 2.0 3503 | 11 2.0 3502       | 174 11 2.0 3502<br>175 11 2.0 3502 | 172 11 2.0 3502<br>173 11 2.0 3502     |
| 111 2.0                                                                                                        | 237 11 2.0 3528 7 1<br>238 11 2.0 3528 7 1<br>239 11 2.0 3528 7 1 | 235 11 2.0 3526 7 1<br>236 11 2.0 3526 7 1 | 234 11 2.0 3525 7                  | 232 11 2.0 3524 7 1 | 230 11 2.0 3524 7 1<br>231 11 2.0 3524 7 1 | 229 11 2.0 3523 7 1 | 227 11 2.0 3522 7 1 | 226 11 2.0 3521 7 1 | 224 11 2.0 3520 7 1                | 223 11 2.0 3520 7 1 | 221 11 2.0 3519 7 (<br>222 11 2.0 3519 7 ( | 220 11 2.0 3519 7 1 | 219 11 2.0 3519 7 1 | 217 11 2.0 3518 7 0 | 216 11 2.0 3518 7 1 | 214 11 2.0 3514 7 ( | 213 11 2.0 3513 7 1 | 211 11 2.0 3512 7 [ | 209 11 2.0 3512 7 U                | 207 11 2.0 3512 7 t<br>208 11 2.0 3512 7 t | 206 11 2.0 3512 7 1 | 204 11 2.0 3511 7 U                | 202 11 2.0 3511 7 0      | 11 2.0 3511 7 1 | 11 2.0 3510 7 t            | 11 2.0 3510 7 1 | 11 2.0 3509 7 L | 11 2.0 3508 7 1 | 11 2.0 3508 7 1 | 11 2.0 3507 7 U            | 11 2.0 3507 7 1 | 11 2.0 3507 7 L  | 11 2.0 3507 7 ( | 11 2.0 3506 7 U | 11 2.0 3505 7 U            | 11 2.0 3504 7 ( | 11 2.0 3504 7 t            | 11 2.0 3503 7 1 | 11 2.0 3503 / C            | 11 2.0 3502 7 U   | 174 11 2.0 3502 7 U                | 173 11 2.0 3502 7 1                    |

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|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------|-------------------------------------------|------------------------------------------|---------------------------------------------------------------------------------------|------------------------------------------|-------------------------------------------|-------------------------------------------|-------------------------------------------|----------------------------------------------|-------------------------------------------|------------------------------------------|----------------------------------------------|-------------------------------------------|-------------------------------------------|-------------------------------------------|----------------------------------------------|------------------------------------------|------------------------------------------|--------------------------------------------------------------------------------------|--------------------------------------------|------------------------------------------|----------------------------------------|-------------------------------------------|--------------------------------------------|-------------------------------------------|----------------------------------------------------------------------------------|------------------------------------------|-----------------------------------------|-----------------------------------------|------------------------------------------|------------------------------------------|--------------------------------------------|--------------------------------------------|--------------------------------------------|--------------------------------------------|----------------------------------------------------------|--------------------------------------------|--------------------------------------------|-------------------------------------------|--------------------------------------------|--------------------------------------------|--------------------------------------------|
| 313<br>314<br>315<br>316                                                                                                                                                      | 311<br>312                                                                                                                        | 309                                                                                    | 307                                                                                    | 305                                       | 303<br>304                               | 302                                                                                   | 9 8                                      | 99                                        | 97<br>98                                  | 96                                        | 4 20                                         | 2 2                                       | 92                                       | 91                                           | 8 9                                       | 288                                       | 3 8                                       | 25 T                                         | 88                                       | 9 2                                      | 80                                                                                   | 278                                        | 77                                       | 75                                     | 273<br>274                                | 272                                        | 270                                       | 2 A<br>6 B<br>8 C<br>8 C<br>8 C<br>8 C<br>8 C<br>8 C<br>8 C<br>8 C<br>8 C<br>8 C | 267                                      | ο ο<br>ο ο                              | 264                                     | 63                                       | 261                                      | 60                                         | 5 8                                        | 57                                         | 255                                        | 254                                                      | 20.00                                      | 251                                        | 250                                       | 249                                        | 7                                          | σ                                          |
| 51000                                                                                                                                                                         | 100                                                                                                                               | 16                                                                                     | 10                                                                                     | 100                                       | 10                                       | 10                                                                                    | 10                                       | 10                                        | 10                                        | 10                                        | 10                                           | 10                                        | 10                                       | 10                                           | 10                                        | 10                                        | 10                                        | 10                                           | 11                                       | : ::                                     | 11                                                                                   | ::                                         | 11                                       | 11                                     | 11                                        | 11 1                                       | 11                                        | 11                                                                               | <b>:</b> :                               | 1 11                                    | 11                                      | 11                                       | 11                                       | 111                                        | 11                                         | 11                                         | ::                                         | 11;                                                      | : :                                        | : 11                                       | 11                                        | 11                                         | :::                                        | 11                                         |
|                                                                                                                                                                               |                                                                                                                                   |                                                                                        |                                                                                        |                                           |                                          |                                                                                       |                                          |                                           |                                           |                                           |                                              |                                           |                                          |                                              |                                           |                                           |                                           |                                              |                                          |                                          |                                                                                      |                                            |                                          |                                        |                                           |                                            |                                           |                                                                                  |                                          |                                         |                                         |                                          |                                          |                                            |                                            |                                            |                                            |                                                          | _                                          | _                                          |                                           |                                            | -                                          | 2.0                                        |
| 1363<br>1363<br>1457                                                                                                                                                          | 1306<br>1348<br>1355                                                                                                              | 1298                                                                                   | 1192                                                                                   | 1061                                      | 1042                                     | 1005                                                                                  | 445                                      | 427                                       | 395                                       | 394                                       | 335<br>340                                   | 320                                       | 299                                      | 259                                          | 217                                       | 145                                       | 127                                       | 3769<br>29                                   | 3742                                     | 3729                                     | 3711                                                                                 | 3661                                       | 3660                                     | 3657                                   | 3650                                      | 3617                                       | 3601                                      | 3599                                                                             | 3595                                     | 262t<br>885t                            | 3587                                    | 3575                                     | 3573                                     | 3561                                       | 3551                                       | 3544<br>3544                               | 3544                                       | 3541                                                     | 3537                                       | 3537                                       | 3537                                      | 3534<br>4534                               | 3533                                       | 3531                                       |
| 17777                                                                                                                                                                         |                                                                                                                                   |                                                                                        |                                                                                        |                                           |                                          |                                                                                       |                                          |                                           |                                           |                                           |                                              |                                           |                                          |                                              |                                           |                                           |                                           |                                              |                                          |                                          |                                                                                      |                                            |                                          |                                        |                                           |                                            |                                           |                                                                                  |                                          |                                         |                                         |                                          |                                          |                                            |                                            |                                            |                                            |                                                          |                                            |                                            |                                           |                                            |                                            |                                            |
|                                                                                                                                                                               | -11-174-<br>-11-174-                                                                                                              | 11-174-                                                                                | 11-174-                                                                                | 11-174-                                   | 11-174-                                  | 11-174-                                                                               | 10-953-                                  | 10-953-                                   | -11-056-                                  | -11-056-                                  | -10-374-<br>-10-953-                         | -11-056-                                  | 10-953-                                  | -10-953-                                     | -10-953-                                  | -10-953-                                  | -10-953-                                  | -11-063-<br>-11-134-                         | -11-063-                                 | -11-063-                                 | -11-063-                                                                             | -11-063-                                   | -11-063-<br>-11-063-                     | -11-063-                               | -11-063-                                  | -11-063-                                   | -11-063-                                  | -11-063-                                                                         | -11-063-                                 | -11-063-                                | -11-063-                                | -11-063-                                 | -11-063-                                 | -11-063-<br>-11-063-                       | -11-063-                                   | -11-063-                                   | -11-063-                                   | -11-063-                                                 | -11-063-                                   | -11-063-                                   | -11-063-                                  | -11-063-                                   | -11-063-                                   | -11-063-                                   |
| Sequence 358,<br>Sequence 2430,<br>Sequence 1094,<br>Sequence 880,                                                                                                            | 288                                                                                                                               | 154<br>277                                                                             | 183                                                                                    | 328                                       | 356                                      | 115                                                                                   | 24                                       | 243                                       | 415                                       | 415                                       | 206                                          | 417                                       | 100                                      | 105                                          | 108                                       | 105                                       | 410                                       | 285                                          | 283                                      | 274                                      | 263                                                                                  | 282                                        | 26                                       | 125                                    | 28                                        | 28.2                                       | 26                                        | 27                                                                               | 26                                       | 2 5                                     | 260                                     | 27.                                      | 15                                       | 12                                         | 13                                         | 9 5                                        | 15                                         | 22                                                       | 23                                         | 1                                          | 7 1                                       | בן ב                                       | 14                                         | 28                                         |
| ), App<br>(0, Ap<br>14, Ap<br>App                                                                                                                                             | 566                                                                                                                               | ซ์ซ์                                                                                   | ซ์ซั                                                                                   | ਰ ਦ                                       | ğğ                                       | ช์ ซั                                                                                 | Þ:                                       | > ×                                       | > ⊅                                       | >:                                        | ⊅ซ์                                          | Þ                                         | > :                                      | <b>&gt;</b> >                                | ≯જે                                       | ว์ >>                                     | י סיי                                     | ชีซี                                         | 7                                        | 88                                       | 9 9                                                                                  | ; <del>;</del> ;                           | 8.8                                      | 9 6                                    | 3 ig ;                                    | 8.8                                        | 9 6                                       | 9.59                                                                             | 8 6                                      | 3 2                                     | gg.                                     | , g                                      | 9.6                                      | 8.8                                        | op ?                                       | 9 9                                        | g;                                         | 9.6                                                      | độ                                         | g                                          | 1:                                        | 7.B                                        | ,<br>L                                     | 8                                          |
| •                                                                                                                                                                             |                                                                                                                                   |                                                                                        |                                                                                        |                                           |                                          |                                                                                       |                                          |                                           |                                           |                                           |                                              |                                           |                                          |                                              |                                           |                                           |                                           |                                              |                                          |                                          |                                                                                      |                                            |                                          |                                        |                                           |                                            |                                           |                                                                                  |                                          |                                         |                                         |                                          |                                          |                                            |                                            |                                            |                                            |                                                          |                                            |                                            |                                           |                                            |                                            |                                            |
| 387<br>388<br>389                                                                                                                                                             | 383<br>384<br>387                                                                                                                 | 381<br>382                                                                             | 380                                                                                    | 378                                       | 376                                      | 374<br>375                                                                            | 373                                      | 372                                       | 370                                       | 369                                       | 367                                          | 366                                       | 365                                      | 363                                          | 362                                       | 360                                       | 359                                       | 357<br>358                                   | 356                                      | 354                                      | 353                                                                                  | 351                                        | 349                                      | 348                                    | 346                                       | 344                                        | 343                                       | 341                                                                              | 340                                      | 338                                     | 337                                     | 335                                      | 334                                      | 332                                        | 331                                        | 329                                        | 328                                        | 325                                                      | 325                                        | 324                                        | 323                                       | 321                                        | 320                                        | 319                                        |
| 3333333<br>38887<br>60887                                                                                                                                                     |                                                                                                                                   |                                                                                        |                                                                                        |                                           |                                          |                                                                                       |                                          |                                           |                                           |                                           |                                              |                                           |                                          |                                              |                                           |                                           |                                           |                                              |                                          |                                          |                                                                                      |                                            |                                          |                                        |                                           |                                            |                                           |                                                                                  |                                          |                                         |                                         |                                          |                                          | _                                          |                                            |                                            |                                            |                                                          |                                            |                                            |                                           |                                            | _                                          |                                            |
| , o o o o o                                                                                                                                                                   | 999                                                                                                                               | 9 9<br>1.1                                                                             | 9 1.                                                                                   | 9 9                                       | 9 1.                                     | 9<br>9<br>1.                                                                          | 9 .                                      | 9 4                                       | 9                                         | 9 .                                       | o 9                                          | 9 1.                                      | 9 .                                      | 9 9                                          | 9 1.                                      | 。<br>9                                    | 9 1 1                                     | o                                            | 9 1.                                     | 9 1.                                     | 9 4                                                                                  | 99                                         | 99                                       | 9 1                                    | 9 9                                       | و و                                        | 9 1.                                      | 9 9                                                                              | 94                                       | 9 9                                     | 9 4                                     | • •                                      | 9 4                                      | 10 1                                       | 10 1                                       | 10 1                                       | 10 1                                       | 10 1                                                     | 10 1                                       | 10 1                                       | 10                                        | 10 1                                       | 10 1                                       | 10 1                                       |
| 9 1.6 1806<br>9 1.6 1811<br>9 1.6 1818<br>9 1.6 1851                                                                                                                          | 9 1.6 1739<br>9 1.6 1771<br>9 1 6 1775                                                                                            | 9 1.6 1696<br>9 1.6 1712                                                               | 9 1.6 1693                                                                             | 9 1.6 1674                                | 9 1.6 1600                               | 9 1.6 1577<br>9 1.6 1598                                                              | 9 1.6 1510                               | 9 1.6 1509<br>9 1.6 1509                  | 9 1.6 1469                                | 9 1.6 1462                                | 9 1.6 1459                                   | 9 1.6 1456                                | 9 1.6 1413                               | 9 1.6 1318                                   | 9 1.6 1313                                | 9 1.6 1293                                | 9 1.6 1199                                | 9 1.6 1098                                   | 9 1.6 1065                               | 9 1.6 845                                | 9 1.6 586                                                                            | 9 1.6 490                                  | 9 1.6 490                                | 9 1.6 463                              | 9 1.6 352                                 | 9 1.6 324                                  | 9 1.6 315                                 | 9 1.6 313                                                                        | 9 1.6 313                                | 9 1.6 224                               | 9 1.6 176                               | 9 1.6 101                                | 9 1.6 100                                | 10 1.8 3392                                | 10 1.8 2328                                | 10 1.8 2016                                | 10 1.8 1942                                | 10 1.8 1933                                              | 10 1.8 1847                                | 10 1.8 1696                                | 10 1.8 1684<br>10 1.8 1684                | 10 1.8 1575                                | 10 1.8 1550                                | 10 1.8 1540                                |
| 9 1.6 1806 7 US-1<br>9 1.6 1811 7 US-1<br>9 1.6 1818 7 US-1<br>9 1.6 1851 7 US-1                                                                                              | 9 1.6 1739 7 US-1<br>9 1.6 1771 7 US-1<br>9 1 6 1775 7 US-1                                                                       | 9 1.6 1696 7 US-1<br>9 1.6 1712 7 US-1                                                 | 9 1.6 1686 7 US-1<br>9 1.6 1693 7 US-1                                                 | 9 1.6 1674 7 US-1                         | 9 1.6 1600 7 US-1                        | 9 1.6 1577 7 US-1<br>9 1.6 1598 7 US-1                                                | 9 1.6 1510 7 US-1                        | 9 1.6 1509 7 US-1                         | 9 1.6 1469 7 US-1                         | 9 1.6 1462 7 US-1                         | 9 1.6 1459 7 US-1                            | 9 1.6 1456 7 US-1                         | 9 1.6 1413 7 US-1                        | 9 1.6 1318 7 US-1                            | 9 1.6 1313 7 US-1                         | 9 1.6 1293 6 US-1                         | 9 1.6 1199 7 US-                          | 9 1.6 1098 7 US-:                            | 9 1.6 1065 7 US-                         | 9 1.6 845 7 US-                          | 9 1.6 586 6 US-<br>9 1.6 785 7 US-                                                   | 9 1.6 490 6 US-                            | 9 1.6 490 6 US-                          | 9 1.6 463 7 US-                        | 9 1.6 352 7 US-                           | 9 1.6 324 6 US-                            | 9 1.6 315 7 US-                           | 9 1.6 313 6 US-                                                                  | 9 1.6 313 6 US-                          | 9 1.6 224 6 US-                         | 9 1.6 176 6 US-                         | 9 1.6 101 6 US-                          | 9 1.6 100 6 US-                          | 10 1.8 3392 7 US-                          | 10 1.8 2328 7 US-                          | 10 1.8 2016 7 US-                          | 10 1.8 1942 7 US-                          | 10 1.8 1917 7 US-                                        | 10 1.8 1847 7 US-                          | 10 1.8 1696 7 US-                          | 10 1.8 1684 7 US-                         | 10 1.8 1575 7 US-                          | 10 1.8 1550 7 US-                          | 10 1.8 1540 7 US-                          |
| 9 1.6 1806 7 US-11-1<br>9 1.6 1811 7 US-11-1<br>9 1.6 1818 7 US-11-1<br>9 1.6 1851 7 US-11-1                                                                                  | 9 1.6 1739 7 US-11-1<br>9 1.6 1771 7 US-11-1<br>9 1 6 1775 7 US-11-1                                                              | 9 1.6 1696 7 US-11-1<br>9 1.6 1712 7 US-11-1                                           | 9 1.6 1686 7 US-11-1<br>9 1.6 1693 7 US-11-1                                           | 9 1.6 1674 7 US-11-1                      | 9 1.6 1600 7 US-11-1                     | 9 1.6 1577 7 US-11-1<br>9 1.6 1598 7 US-11-1                                          | 9 1.6 1510 7 US-11-1                     | 9 1.6 1509 7 US-11-1                      | 9 1.6 1469 7 US-11-1                      | 9 1.6 1462 7 US-11-1                      | 9 1.6 1459 7 US-11-1<br>9 1.6 1460 7 US-11-1 | 9 1.6 1456 7 US-11-1                      | 9 1.6 1413 7 US-11-1                     | 9 1.6 1318 7 US-11-1<br>9 1 6 1336 7 US-11-1 | 9 1.6 1313 7 US-11-1                      | 9 1.6 1293 6 US-10-4                      | 9 1.6 1199 7 US-11-1                      | 9 1.6 1098 7 US-11-1<br>9 1.6 1162 7 US-11-1 | 9 1.6 1065 7 US-11-1                     | 9 1.6 845 7 US-11-1                      | 9 1.6 785 7 US-11-3                                                                  | 9 1.6 490 6 · US-10-4                      | 9 1.6 490 6 US-10-4                      | 9 1.6 463 7 US-11-1                    | 9 1.6 352 7 US-11-0                       | 9 1.6 324 6 US-10-9<br>9 1.6 324 7 US-11-0 | 9 1.6 315 7 US-11-0                       | 9 1.6 313 6 US-10-4                                                              | 9 1.6 313 6 US-10-4                      | 9 1.6 224 6 US-10-9                     | 9 1.6 176 6 US-10-9                     | 9 1.6 101 6 US-10-9                      | 9 1.6 100 6 US-10-9                      | 10 1.8 3392 7 US-11-1                      | 10 1.8 2328 7 US-11-1                      | 10 1.8 2016 7 US-11-1                      | 10 1.8 1942 7 US-11-1                      | 10 1.8 1917 7 US-11-1<br>10 1.8 1933 7 US-11-1           | 10 1.8 1847 7 US-11-1                      | 10 1.8 1696 7 US-11-1                      | 10 1.8 1684 7 US-11-1                     | 10 1.8 1575 7 US-11-1                      | 10 1.8 1550 7 US-11-1                      | 10 1.8 1540 7 US-11-1                      |
| 9 1.6 1806 7 US-11-1<br>9 1.6 1811 7 US-11-1<br>9 1.6 1818 7 US-11-1<br>9 1.6 1851 7 US-11-1                                                                                  | 9 1.6 1739 7 US-11-174-307<br>9 1.6 1771 7 US-11-174-307<br>9 1 6 1775 7 US-11-174-307                                            | 9 1.6 1696 7 US-11-174-307<br>9 1.6 1712 7 US-11-174-307                               | 9 1.6 1686 7 US-11-174-307<br>9 1.6 1693 7 US-11-174-307                               | 9 1.6 1674 7 US-11-174-307                | 9 1.6 1600 7 US-11-174-307               | 9 1.6 1577 7 US-11-174-307<br>9 1.6 1598 7 US-11-174-307                              | 9 1.6 1510 7 US-11-174-30                | 9 1.6 1509 7 US-11-174-30                 | 9 1.6 1469 7 US-11-174-307                | 9 1.6 1462 7 US-11-174-30                 | 9 1.6 1459 7 US-11-174-30                    | 9 1.6 1456 7 US-11-174-307                | 9 1.6 1413 7 US-11-174-30                | 9 1.6 1318 7 US-11-174-307                   | 9 1.6 1313 7 US-11-174-30                 | 9 1.6 1293 6 US-10-449-903                | 9 1.6 1199 7 US-11-174-30                 | 9 1.6 1098 7 US-11-174-30                    | 9 1.6 1065 7 US-11-174-30                | 9 1.6 845 7 US-11-174-30                 | 9 1.6 586 6 US-10-449-903<br>9 1.6 785 7 US-11-330-403                               | 9 1.6 490 6 US-10-449-90                   | 9 1.6 490 6 US-10-449-90:                | 9 1.6 463 7 US-11-174-30               | 9 1.6 352 7 US-11-056-35                  | 9 1.6 324 6 US-10-953-349                  | 9 1.6 315 7 US-11-056-35                  | 9 1.6 313 6 US-10-449-90                                                         | 9 1.6 313 6 US-10-449-90                 | 9 1.6 224 6 US-10-953-34                | 9 1.6 176 6 US-10-953-34                | 9 1.6 101 6 US-10-953-34                 | 9 1.6 100 6 US-10-953-34                 | 10 1.8 3392 7 US-11-174-30                 | 10 1.8 2328 7 US-11-174-30                 | 10 1.8 2016 7 US-11-174-30                 | 10 1.8 1942 7 US-11-174-30                 | 10 1.8 1917 7 US-11-174-30<br>10 1.8 1933 7 US-11-174-30 | 10 1.8 1847 7 US-11-174-30                 | 10 1.8 1696 7 US-11-174-30                 | 10 1.8 1684 7 US-11-174-30                | 10 1.8 1575 7 US-11-174-30                 | 10 1.8 1550 7 US-11-174-30                 | 10 1.8 1540 7 US-11-174-30                 |
| 9 1.6 1806 7 US-11-174-307B-872 Sequence<br>9 1.6 1811 7 US-11-174-307B-924 Sequence<br>9 1.6 1818 7 US-11-174-307B-586 Sequence<br>9 1.6 1818 7 US-11-174-307B-2240 Sequence | 9 1.6 1739 7 US-11-174-307B-3342 Sequence<br>9 1.6 1771 7 US-11-174-307B-928 Sequence<br>9 1.6 1775 7 US-11-174-307B-526 Sequence | 9 1.6 1696 7 US-11-174-307B-1464 Sequence<br>9 1.6 1712 7 US-11-174-307B-1086 Sequence | 9 1.6 1686 7 US-11-174-307B-1802 Sequence<br>9 1.6 1693 7 US-11-174-307B-4190 Sequence | 9 1.6 1674 7 US-11-174-307B-1328 Sequence | 9 1.6 1600 7 US-11-174-307B-636 Sequence | 9 1.6 1577 7 US-11-174-307B-396 Sequence<br>9 1.6 1598 7 US-11-174-307B-2072 Sequence | 9 1.6 1510 7 US-11-174-307B-838 Sequence | 9 1.6 1509 7 US-11-174-307B-1838 Segmence | 9 1.6 1469 7 US-11-174-307B-1890 Sequence | 9 1.6 1462 7 US-11-174-307B-1056 Sequence | 9 1.6 1459 7 US-11-174-307B-1350 Sequence    | 9 1.6 1456 7 US-11-174-307B-1164 Sequence | 9 1.6 1413 7 US-11-174-307B-936 Sequence | 9 1.6 1318 7 US-11-174-307B-2184 Sequence    | 9 1.6 1313 7 US-11-174-307B-2312 Sequence | 9 1.6 1293 6 US-10-449-902-41380 Sequence | 9 1.6 1199 7 US-11-174-307B-2390 Sequence | 9 1.6 1098 7 US-11-174-307B-2006 Sequence    | 9 1.6 1065 7 US-11-174-307B-370 Sequence | 9 1.6 845 7 US-11-174-307B-1232 Sequence | 9 1.6 586 6 US-10-449-902-37943 Sequence<br>9 1.6 785 7 US-11-330-403-16179 Sequence | 9 1.6 490 6 · US-10-449-902-50471 Sequence | 9 1.6 490 6 US-10-449-902-28793 Sequence | 9 1.6 463 7 US-11-174-307B-80 Sequence | 9 1.6 352 7 US-11-056-355B-68835 Sequence | 9 1.6 324 6 US-10-953-349-17977 Sequence   | 9 1.6 315 7 US-11-056-355B-58249 Sequence | 9 1.6 313 6 US-10-449-902-54725 Sequence                                         | 9 1.6 313 6 US-10-449-902-45378 Sequence | 9 1.6 224 6 US-10-953-349-7024 Sequence | 9 1.6 176 6 US-10-953-349-7025 Sequence | 9 1.6 101 6 US-10-953-349-35939 Sequence | 9 1.6 100 6 US-10-953-349-35941 Sequence | 10 1.8 3392 7 US-11-174-307B-1654 Sequence | 10 1.8 2328 7 US-11-174-307B-1936 Sequence | 10 1.8 2016 7 US-11-174-307B-1352 Sequence | 10 1.8 1942 7 US-11-174-307B-1096 Sequence | 10 1.8 1917 / US-11-174-307B-2172 Sequence               | 10 1.8 1847 7 US-11-174-307B-2852 Sequence | 10 1.8 1696 7 US-11-174-307B-3178 Sequence | 10 1.8 1684 7 US-11-174-307B-402 Seguence | 10 1.8 1575 7 US-11-174-307B-2648 Sequence | 10 1.8 1550 7 US-11-174-307B-2158 Sequence | 10 1.8 1540 7 US-11-174-307B-2428 Sequence |
| 9 1.6 1806 7 US-11-174-307<br>9 1.6 1811 7 US-11-174-307<br>9 1.6 1818 7 US-11-174-307<br>9 1.6 1851 7 US-11-174-307                                                          | 9 1.6 1739 7 US-11-174-307B-3342 Sequence<br>9 1.6 1771 7 US-11-174-307B-928 Sequence<br>9 1.6 1775 7 US-11-174-307B-526 Sequence | 9 1.6 1696 7 US-11-174-307B-1464 Sequence<br>9 1.6 1712 7 US-11-174-307B-1086 Sequence | 9 1.6 1686 7 US-11-174-307B-1802 Sequence<br>9 1.6 1693 7 US-11-174-307B-4190 Sequence | 9 1.6 1674 7 US-11-174-307B-1328 Sequence | 9 1.6 1600 7 US-11-174-307B-636 Sequence | 9 1.6 1577 7 US-11-174-307B-396 Sequence<br>9 1.6 1598 7 US-11-174-307B-2072 Sequence | 9 1.6 1510 7 US-11-174-307B-838 Sequence | 9 1.6 1509 7 US-11-174-307B-1838 Segmence | 9 1.6 1469 7 US-11-174-307B-1890 Sequence | 9 1.6 1462 7 US-11-174-307B-1056 Sequence | 9 1.6 1459 7 US-11-174-307B-1350 Sequence    | 9 1.6 1456 7 US-11-174-307B-1164 Sequence | 9 1.6 1413 7 US-11-174-307B-936 Sequence | 9 1.6 1318 7 US-11-174-307B-2184 Sequence    | 9 1.6 1313 7 US-11-174-307B-2312 Sequence | 9 1.6 1293 6 US-10-449-902-41380 Sequence | 9 1.6 1199 7 US-11-174-307B-2390 Sequence | 9 1.6 1098 7 US-11-174-307B-2006 Sequence    | 9 1.6 1065 7 US-11-174-307B-370 Sequence | 9 1.6 845 7 US-11-174-307B-1232 Sequence | 9 1.6 586 6 US-10-449-902-37943 Sequence<br>9 1.6 785 7 US-11-330-403-16179 Sequence | 9 1.6 490 6 · US-10-449-902-50471 Sequence | 9 1.6 490 6 US-10-449-902-28793 Sequence | 9 1.6 463 7 US-11-174-307B-80 Sequence | 9 1.6 352 7 US-11-056-355B-68835 Sequence | 9 1.6 324 6 US-10-953-349-17977 Sequence   | 9 1.6 315 7 US-11-056-355B-58249 Sequence | 9 1.6 313 6 US-10-449-902-54725 Sequence                                         | 9 1.6 313 6 US-10-449-902-45378 Sequence | 9 1.6 224 6 US-10-953-349-7024 Sequence | 9 1.6 176 6 US-10-953-349-7025 Sequence | 9 1.6 101 6 US-10-953-349-35939 Sequence | 9 1.6 100 6 US-10-953-349-35941 Sequence | 10 1.8 3392 7 US-11-174-307B-1654 Sequence | 10 1.8 2328 7 US-11-174-307B-1936 Sequence | 10 1.8 2016 7 US-11-174-307B-1352 Sequence | 10 1.8 1942 7 US-11-174-307B-1096 Sequence | 10 1.8 1917 / US-11-174-307B-2172 Sequence               | 10 1.8 1847 7 US-11-174-307B-2852 Sequence | 10 1.8 1696 7 US-11-174-307B-3178 Sequence | 10 1.8 1684 7 US-11-174-307B-402 Seguence | 10 1.8 1575 7 US-11-174-307B-2648 Sequence | 10 1.8 1550 7 US-11-174-307B-2158 Sequence | 10 1.8 1540 7 US-11-174-307B-2428 Sequence |

| 461<br>462                                                             | 460      | 458<br>608 | 457       | 455               | 454         | 452        | 451       | 450       | 449       | 447          | 446       | 445       | 443       | 442      | 441       | 440            | 439         | 437         | 436       | 435      | 43 U         | 433        | 431            | 430            | 428                  | 427               | 426                              | 424               | 423                  | 421                  | 420                  | 419       | 418                  | 416                 | 415                 | 413<br>414 | 412                 | 411            | 409                  | 408                  | 407                  | 406                              | 404                 | 403                 | 402                 | 400                 | 399                  | 398                  | 397                  | 3 9 5<br>6 5         | 394                 | 393                 | 392           |
|------------------------------------------------------------------------|----------|------------|-----------|-------------------|-------------|------------|-----------|-----------|-----------|--------------|-----------|-----------|-----------|----------|-----------|----------------|-------------|-------------|-----------|----------|--------------|------------|----------------|----------------|----------------------|-------------------|----------------------------------|-------------------|----------------------|----------------------|----------------------|-----------|----------------------|---------------------|---------------------|------------|---------------------|----------------|----------------------|----------------------|----------------------|----------------------------------|---------------------|---------------------|---------------------|---------------------|----------------------|----------------------|----------------------|----------------------|---------------------|---------------------|---------------|
| 0000                                                                   | ω (      | 0 00       | 80 (      | 30 CC             | <b>co</b> c | no 00      | · œ       | 80        | œ c       | <b>10</b> 00 | . &       | œ (       | oo oo     | တ        | 80        | <b>&amp;</b> ( | <b>oo</b> c | n co        | တ         | 80       | <b>o</b> o o | o 00       | ω (            | œ c            | <b>D</b> CO          | 8                 | 30 CC                            | œ                 | œ (                  | 20 00                | ω                    | ω (       | œ o                  | o 00                | œ ·                 | 00 00      | ω.                  | œ o            | 0 00                 | œ                    | ω (                  | ao a                             | 000                 | 8                   | œ (                 | 20 OC               | o o                  | 9                    | 9 4                  | ο                    | 9                   | 9                   | 9             |
| 11.4                                                                   | 1.4      |            |           |                   | 1.4         |            |           |           |           |              |           |           |           |          |           |                |             |             |           |          |              |            |                |                |                      |                   |                                  |                   |                      |                      |                      |           |                      |                     |                     |            |                     |                | •                    |                      |                      |                                  |                     |                     |                     |                     | •                    |                      |                      | •                    | •                   |                     | •             |
| 484<br>505                                                             | 484      | 466        | 464       | 4 4<br>0 0<br>4 4 | 451         | 434        | 434       | 430       | 430       | 422          | 420       | 420       | 416       | 412      | 411       | 399            | 389         | 376         | 368       | 360      | 359          | 0 G        | 357            | 357            | 323                  | 323               | 318                              | 311               | 311                  | 307<br>209           | 254                  | 246       | 246                  | 232                 | 232                 | 232        | 204                 | 204            | 204                  | 204                  | 204                  | 202                              | 198                 | 198                 | 179                 | 22.0                | 4243                 | 2143                 | 2142                 | 2003                 | 1962                | 1957                | 1951          |
| 7 US                                                                   |          |            |           |                   |             |            |           |           |           |              |           |           |           |          |           |                |             |             |           |          |              |            |                |                |                      |                   |                                  |                   |                      |                      |                      |           |                      |                     |                     |            |                     |                |                      |                      |                      |                                  |                     |                     |                     |                     |                      |                      |                      |                      |                     |                     |               |
| /S-10-449-902-45190<br>/S-11-330-403-611                               | -10-449- | -11-056-   | -11-056-  | -10-953-          | -11-056-    | -11-056-   | -11-056-  | -11-056-  | -10-953-  | -10-449-     | -11-056-  | -10-449-  | -10-449-  | -10-953- | -10-449-  | -10-449-       | -11-056-    | -11-056-    | -10-449-  | -11-056- | -11-056-     | -10-449-   | -11-056-       | -11-056-       | -11-056-<br>-10-449- | -10-374-780A-2178 | -11-056-                         | -11-056-355B-8006 | -10-449-             | -11-056-             | -10-566-             | -10-449-  | -10-449-             | -11-056-355B-98416  | -11-056-            | -11-056-   | -11-056-            | -11-056-       | -11-056-             | -11-056-             | -11-056-             | -11-056-                         | -11-056-            | -11-056-            | -11-330-            | -10-449-            | -11-174-             | -11-174-             | -11-174-             | -11-174-             | -11-174-            | -11-174-            | -11-174-      |
| Sequence 45190,<br>Sequence 611, Ap                                    | equence  | equence    | equence ! | equence           | equence     | equence    | equence : | equence ! | equence : | equence :    | equence ( | equence , | equence : | equence  | equence : | equence ,      | equence (   | equence :   | equence : | equence  | equence ;    | equence .  | equence 109654 | equence 98415, | equence (            | equence 2178,     | equence 101841<br>equence 113080 | equence 80069     | equence 36926        | equence 19575        | equence 322,         | equence ! | equence 103038       | equence 98416       | equence 71348       | equence (  | equence 10965       | equence /1349, | equence 50009,       | equence 32191,       | equence 28601,       | equence 2856/,<br>equence 32157. | equence 32158,      | equence 28568,      | equence 18758,      | equence 54, Ap      | equence 1722,        | equence 2550,        | equence 1434,        | equence !            | equence 1446,       | equence 2230,       | equence 3118, |
|                                                                        |          | -          |           |                   |             |            |           |           |           |              |           |           |           |          |           |                |             |             |           |          |              |            |                |                |                      |                   |                                  |                   |                      |                      |                      |           |                      |                     |                     |            |                     |                |                      |                      |                      |                                  |                     |                     |                     |                     |                      |                      |                      |                      |                     |                     |               |
| 534<br>535                                                             | 533      | 531        | 530       | 528               | 527         | 500        | 524       | 523       | 522       | 520          | 519       | 518       | 517       | 515      | 514       | 513            | 512         | 510         | 509       | 508      | 507          | 10 C       | 504            | 503            | 501                  | 500               | 499                              | 497               | 496                  | 494                  | 493                  | 492       | 491                  | 189                 | 488                 | 486<br>487 | 485                 | 484            | 482                  | 481                  | 480                  | 479                              | 477                 | 476                 | 475                 | 474                 | 472                  | 471                  | 470                  | 168                  | 167                 | 166                 | 275           |
| 0 00 00                                                                |          |            | 80        |                   | 00 0        | 000        | 000       | 80        | ω (       | <b>20 00</b> | 000       | 80        | œ α       | - α      |           | œ (            | œ (         | 20 00       |           | 80       | œ c          | ο α        | 00             | 00 (           | 2000                 | 00                | ο σ                              |                   | ω (                  | ο α                  | 000                  | 80 (      | 000                  |                     |                     | 8 8        |                     |                |                      |                      |                      |                                  |                     |                     |                     |                     |                      |                      |                      |                      |                     |                     |               |
| 44.                                                                    | .44,     | 4, 4       |           |                   | -           |            | -         |           |           |              |           |           |           |          |           |                |             |             |           |          |              |            | -              |                | 4.4                  | ,,                |                                  | - "               |                      |                      |                      |           | 4.                   | 4.                  | 4                   | 44         | .4                  |                | 4.                   | .4                   | .4                   | <br>4 4                          | 4. 4                | .4                  | . 4.                | 4.4                 | 4٠                   | .4                   |                      | 4. 4                 | 4.                  | 4                   |               |
| 1443 7<br>1449 7                                                       | υı       | بر د       | 9         | N U               | 9.          | <b>1</b> 0 | ιω        | G         | 7 (       | <i></i>      | יסי       | N         | oo o      | . 0      | 44        | 9              | 42 (        | <b>&gt;</b> | 1 7       | ы        | .44          | <i>p</i> u | 9              | UT (           | 00                   | 42.               | ωυ                               | או                | 7                    | 7                    | 1 7                  | 7         | 7                    | 1 7                 | 7                   | 7 -        | 1 10                | ww             | o w                  | 9                    | Ψ,                   | vo v                             | φ                   | Ψ                   | Φ                   | <b>35</b> 0.        |                      | ω                    | ш с                  | b 60                 | ω                   | ω.                  | Œ             |
| 7 US-11-174-307B-2906<br>7 US-11-174-307B-134<br>7 IIS-11-174-307B-336 | us-      | II C       | US-       | . SI              | -Sn         | 1 C        | us-       | US-       | US-       | , S          | us-       | US-       | S. S.     | SO-      | us-       | us-            | us-         | , S         | s us      | us-      | ري<br>دي     | 200        | ı ç            | us-            | S                    | us-               | US -                             | -<br>S 5          | US-11-056-355B-11983 | US-11-056-355B-11982 | US-11-056-355B-10859 | us-       | US-11-056-355B-10834 | US-11-056-355B-4714 | US-11-056-355B-4501 | US C       | US-11-174-307B-5524 | g g            | US-11-056-355B-11958 | US-11-056-355B-10859 | US-11-056-355B-10858 | US-11-056-355B-10834             | US-11-056-355B-4714 | US-11-056-355B-4501 | US-10-953-349-10658 | US-11-056-355B-1198 | US-11-056-355B-11958 | US-11-056-355B-10859 | US-11-056-355B-10858 | US-11-056-355B-49869 | US-11-056-355B-4715 | US-11-056-355B-4501 | -Sn           |
| Sequence                                                               | Sequenc  | Sequenc    | Sequenc   | Sequence          | Sequence    | Segueno    | Sequence  | Sequence  | Sequenc   | Seguenc      | Sequenc   | Sequence  | Seguenc   | Sequence | Sequence  | Sequence       | Sequence    | עו ע        | , w       | (U       | (0 (         | V (L       | עו             | י עו           | Sequence 54667       | w                 | וט וו                            | , ,,              | (0)                  | וט עו                | , w                  | יעו       | (V (                 | טו ע                | w                   | וט עו      | · (D                | w              | עו ע                 | עו                   | w                    | ( )                              | ט ע                 | w                   | w                   | Seguence            | ט י                  | w                    | w                    | טו ע                 | w                   | w                   | w             |

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e 2206, Ap e 2416, App e 2416,
 RESULT 2
US-10-953-349-34264
US-10-953-349-34264
; Sequence 34264, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: BECOMED THERBY
 ; ORGANISM: Staphylococcus aureus ; FEATURE; FEATURE; NAME/KEY: MISC FEATURE; LOCATION: (1)...(166); OTHER INFORMATION: hypothetical US-10-471-571A-782
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 RESULT 1
US-10-471-571A-782
 Query Match
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Matches 13
 APPLICANT: CHIRON SpA
TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE: P026927WO
CURRENT APPLICATION NUMBER: US/10/471,571A
CURRENT FILING DATE: 2003-09-12
PRIOR APPLICATION NUMBER: GB-0107661.1
PRIOR FILING DATE: 2001-03-27
PRIOR FILING DATE: 2001-03-27
NUMBER: OF SEQ ID NOS: 5642
SOFTWARE: SegWin99, version 1.03
SEQ ID NO 782
LENGTH: 166
 Sequence 782, Applic Publication No. US20 GENERAL INFORMATION:
 FILE REFERENCE:
 TYPE: PRT
 392 QTTTTTTTTTTTTTS 404
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 Similarity
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 Application US/10471571A
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 ; LENGTH: 659
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-11680
 RESULT 3
US-10-953-349-11680
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 US-10-953-349-34264
 GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
CORTUNEER DESCRIPTION SEQ OF SEQ OF SECONDARY SECONDAR
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Matches
 CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 34264
 SOFTWARE: PatentIn version 3.3 SEQ ID NO 11680
 Sequence 11680, Application US/10953349 Publication No. US20060107345A1
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 FEATURE:
FEATURE:
NAME/KEY: misc_feature
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 FEATURE:
NAME/KEY: misc feature
LOCATION: (215)..(215)
OTHER INFORMATION: Xaa
 NAME/KEY: misc feature LOCATION: (156)..(158) OTHER INFORMATION: Xaa
 TYPE: PRT
ORGANISM: Zea mays subsp. mays
 FEATURE:
NAME/KEY: misc_feature
LOCATION: (177)...(177)
OTHER INFORMATION: Xaa
 NAME/KEY: misc_feature
LOCATION: (165)..(165)
OTHER INFORMATION: Xaa can
 OTHER INFORMATION: Xaa
 NAME/KEY: misc_feature
LOCATION: (204)..(204)
 OTHER INFORMATION: Xaa
 OTHER INFORMATION: Xaa can be any naturally occurring
 NAME/KEY: misc feature LOCATION: (171)..(171)
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RESULT 4
US-11-063-439-66
US-11-063-439-66; Application US/11063439
; Publication No. US20060147371A1
; TYPE: PRT ; ORGANISM: Anemia phyllitidis US-11-063-439-24
 뭐
 US-11-063-439-66
 US-11-063-439-24
 Sequence 24, Application US/11063439 Publication No. US20060147371A1 GENERAL INFORMATION:
 SOFTWARE: PatentIn version 3.3 SEQ ID NO 24
 SEQ ID NO 66
 Matches
 Query Match
 GENERAL INFORMATION:
 APPLICANT: TUSZYNSKI, JACK A.
APPLICANT: GREENWALD, HOWARD
APPLICANT: CURRY, STEPHEN H.
 APPLICANT: TUSZYNSKI, JACK A.
APPLICANT: GREENWALD, HOWARD J.
APPLICANT: CURRY, STEPHEN H.
 PRIOR APPLICATION NUMBER: 10/808,618 PRIOR FILING DATE: 2004-03-24 PRIOR APPLICATION NUMBER: 10/867,517
 FILE REFERENCE: 1034312-000027
CURRENT APPLICATION NUMBER: US/11/063,439
CURRENT FILING DATE: 2005-02-23
 PRIOR APPLICATION NUMBER: 10/867,517
PRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 418
 PRIOR APPLICATION NUMBER: 60/516,134
PRIOR FILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: 10/808,618
PRIOR FILING DATE: 2004-03-24
 CURRENT APPLICATION NUMBER: US/11/063,439
CURRENT FILING DATE: 2005-02-23
PRIOR APPLICATION NUMBER: 10/878,905
 PRIOR APPLICATION NUMBER: 10/923,615
PRIOR FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: 60/516,134
PRIOR FILING DATE: 2003-10-31
 TITLE OF INVENTION: WATER-SOLUBLE COMPOUND FILE REFERENCE: 1034312-000027
 NUMBER OF SEQ ID NOS: 418
 PRIOR FILING DATE: 2004-06-14
 PRIOR APPLICATION NUMBER: 10/878,905 PRIOR FILING DATE: 2004-06-28
 TITLE OF INVENTION: WATER-SOLUBLE COMPOUND
 APPLICANT:
 SOFTWARE:
 PRIOR APPLICATION NUMBER: 10/923,615
PRIOR FILING DATE: 2004-08-20
 LENGTH: 1675
TYPE: PRT
ORGANISM: Pneumocystis carinii
 PRIOR FILING DATE: 2004-06-28
 LENGTH: 2823
 Local Similarity
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 PatentIn version 3.3
 TTTTTTTTTTS 1393
 CURRY, STEPHEN GOSS, KENDRICK
 GOSS, KENDRICK
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 DB 7; Length 1675; 0.014;
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RESULT 7
US-11-063-439-68
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 ; ORGANISM: Zea mays US-11-063-439-273
 FILE REFERENCE: 1034312-000027

CURRENT APPLICATION NUMBER: US/11/063,439

CURRENT FILING DATE: 2005-02-23

PRIOR APPLICATION NUMBER: 10/878,905

PRIOR APPLICATION NUMBER: 10/878,905

PRIOR PILING DATE: 2004-06-28

PRIOR PILING DATE: 2004-08-20

PRIOR PILING DATE: 2004-08-20

PRIOR PILING DATE: 2003-10-31

PRIOR PILING DATE: 2003-10-31

PRIOR APPLICATION NUMBER: 10/808,618

PRIOR PILING DATE: 2004-06-14
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 SOFTWARE: PatentIn version 3.3
SEQ ID NO 273
LENGTH: 3342
 Query Match
Best Local Similarity
 Sequence 273, Appropriate Publication No.
 GENERAL INFORMATION:
 Sequence 68, Application US/11063439 Publication No. US20060147371A1
 Matches 12;
 Query Match
Best Local (
 GENERAL INFORMATION:
 Matches
 APPLICANT: TUSZYNSKI, JACK A. APPLICANT: GREENWALD, HOWARD APPLICANT: CURRY, STEPHEN H.
 APPLICANT: GOSS, KENDRICK
TITLE OF INVENTION: WATER-SOLUBLE COMPOUND
 FILE REFERENCE: 1034312-000027
CURRENT APPLICATION NUMBER: US/11/063,439
CURRENT FILING DATE: 2005-02-23
 APPLICANT: TUSZYNSKI, JACK A.
APPLICANT: GREENWALD, HOWARD J.
APPLICANT: CURRY, STEPHEN H.
APPLICANT: GOSS, KENDRICK
 PRIOR APPLICATION NUMBER: 10/923,615
PRIOR FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: 60/516,134
PRIOR FILING DATE: 2003-10-31
 TITLE OF INVENTION: WATER-SOLUBLE COMPOUND
 PRIOR FILING DATE:
 PRIOR APPLICATION NUMBER: 10/878,905 PRIOR FILING DATE: 2004-06-28
 NUMBER OF SEQ ID NOS: 418
 2541
 APPLICATION NUMBER: 10/867,517
 FILING DATE:
 APPLICATION NUMBER: 10/808,618
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 393 TTTTTTTTTTS 404
 Similarity
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 CURRY, STEPHEN
GOSS, KENDRICK
 Application US/11063439
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 US20060147371A1
NOS:
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 2004-06-14
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 2.2%; Score 12; DB 7; Length 2823; 100.0%; Pred. No. 0.022;
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 DB 7; Length 3342; 0.025;
 0; Indels
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APPLICANT: TUSZYNSKI, JACK A.
APPLICANT: GREENWALD, HOWARD J.
APPLICANT: CURRY, STEPHEN H.
APPLICANT: CURRY, STEPHEN H.
APPLICANT: GOSS, KENDRICK
TITLE OF INVENTION: WATER-SOLUBLE COMPOUND
FILE REFERENCE: 1034312-000027
CURRENT APPLICATION UMBER: US/11/063,439
CURRENT FILING DATE: 2005-02-23
PRIOR APPLICATION NUMBER: 10/878,905
PRIOR APPLICATION NUMBER: 10/923,615
PRIOR APPLICATION NUMBER: 10/923,615
PRIOR FILING DATE: 2004-08-20
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 US-11-063-439-86
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 ; ORGANISM: Schizosaccharomyces pombe US-11-063-439-248
 RESULT 9
 TITLE OF INVENTION: WATER-SOLUBLE COMPOUND FILE REFERENCE: 1034312-000027
CURRENT APPLICATION NUMBER: US/11/063,439
CURRENT FILING DATE: 2005-02-23
PRIOR RELILING DATE: 2004-06-28
PRIOR RELILING DATE: 2004-06-28
PRIOR PPLICATION NUMBER: 10/923,615
PRIOR APPLICATION NUMBER: 00/923,615
PRIOR APPLICATION NUMBER: 05/16,134
PRIOR FILING DATE: 2004-08-20
PRIOR PPLICATION NUMBER: 00/516,134
PRIOR PILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: 10/808,618
PRIOR APPLICATION NUMBER: 10/808,618
PRIOR APPLICATION NUMBER: 10/867,517
PRIOR APPLICATION NUMBER: 10/867,517
PRIOR FILING DATE: 2004-03-24
PRIOR FILING DATE: 2004-06-14
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 ; SOFTWARE: Pate
; SEQ ID NO 248
; LENGTH: 3476
 US-11-063-439-248
 ; ORGANISM: Avena sativa
US-11-063-439-68
 Sequence 86, Application US/11063439 Publication No. US20060147371A1 GENERAL INFORMATION:
 Query Match
Best Local Similarity
Matches 12; Conserv
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Best Local
 GENERAL INFORMATION:
 SOFTWARE: PatentIn version 3.3 SEQ ID NO 68 LENGTH: 3445 TYPE: PRT
 Publication No.
 APPLICANT: TUSZYNSKI, JACK A. APPLICANT: GREENWALD, HOWARD
 NUMBER OF SEQ ID NOS: 418
 APPLICANT: CURRY, STEPHEN H. APPLICANT: GOSS, KENDRICK
 TYPE: PRT
 Local Similarity
les 12; Conserv
 1779 TTTTTTTTTTS 1790
 1831 TITTTTTTTTS 1842
 393 TITTTTTTTTS 404
 393 TTTTTTTTTTS 404
 PatentIn version 3.3
 Application US/11063439
 Conservative
 Conservative
 US20060147371A1
 2.2%; Score 12;
100.0%; Pred. No.
vative 0; Mismatcl
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100.0%; Pred. No.
1tive 0; Mismatcl
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 DB 7;
. 0.026;
 DB 7; Length 3445; 0.026;
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 US-11-063-439-59
 RESULT 11
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 US-11-063-439-10
 US-11-063-439-86
 US-11-063-439-10
 PRIOR APPLICATION NUMBER: 60/516,134
PRIOR FILING DATE: 2003-10-31
PRIOR PPLICATION NUMBER: 10/808,618
PRIOR FILING DATE: 2004-03-24
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 10/867,517
PRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 418
 Sequence 59, Application US/110 Publication No. US20060147371A1 GENERAL INFORMATION:
 SEQ ID NO 86
 SEQ ID NO 10
 Sequence 10, Ap
Publication No.
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 GENERAL INFORMATION:
 PRIOR APPLICATION NUMBER: 60/516,134
PRIOR TILING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: 10/808,618
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 10/867,517
PRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 418
 APPLICANT:
 APPLICANT: TUSZYNSKI, JACK A.
APPLICANT: GREENWALD, HOWARD J.
 FILE REFERENCE: 1034312-000027
CURRENT APPLICATION NUMBER: US/11/063,439
CURRENT FILING DATE: 2005-02-23
 PRIOR APPLICATION NUMBER: 10/878,905
PRIOR FILING DATE: 2004-06-28
PRIOR APPLICATION NUMBER: 10/923,615
PRIOR FILING DATE: 2004-08-20
 APPLICANT: TUSZYNSKI, JACK A. APPLICANT: GREENWALD, HOWARD
 SOFTWARE: PatentIn version 3.3
TITLE OF INVENTION: WATER-SOLUBLE COMPOUND
 SOFTWARE: PatentIn version 3.3
 FILE REFERENCE:
 TITLE OF INVENTION: WATER-SOLUBLE COMPOUND
 LENGTH: 3481
TYPE: PRT
ORGANISM: Physarum polycephalum
 ORGANISM: Hordeum vulgare
 TYPE: PRT
 Local Similarity nes 12; Conserv
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les 12; Conserv
 1834 TTTTTTTTTTS 1845
 1835 TTTTTTTTTTTS 1846
 393 TTTTTTTTTTS 404
 393 TTTTTTTTTTS 404
 3485
 CURRY, STEPHEN H. GOSS, KENDRICK
 GREENWALD, HOWARD J.
 CURRY, STEPHEN H. GOSS, KENDRICK
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 Application US/11063439
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100.0%; Pred. No.
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 2.2%; Score 12;
100.0%; Pred. No.
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0.026;
 DB 7; Length 3485;
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RESULT 12
US-11-063-439-76
; Sequence 76, Application US/11063439
; Publication No. US20060147371A1
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 ; ORGANISM: Physarum polycephalum US-11-063-439-76
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 US-11-063-439-59
 PRIOR APPLICATION NUMBER: 10/923,615
PRIOR FILLING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: 60/516,134
PRIOR FILLING DATE: 2003-10-31
PRIOR FILLING DATE: 2003-10-31
PRIOR APPLICATION NUMBER: 10/808,618
PRIOR APPLICATION NUMBER: 10/807,517
PRIOR PILLING DATE: 2004-08-7,517
PRIOR PILLING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 418
NUMBER OF SEQ ID NOS: 418
 PRIOR APPLICATION NUMBER: 10/878,905
PRIOR FILING DATE: 2004-06-28
PRIOR PPLICATION NUMBER: 10/923,615
PRIOR FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: 60/516,134
PRIOR APPLICATION NUMBER: 10/808,618
PRIOR APPLICATION NUMBER: 10/808,618
 SEQ ID NO 76
 SOFTWARE: Pa
 Matches
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 GENERAL INFORMATION:
 Best Local Similarity Matches 12; Conserv
 Query Match
 APPLICANT: TUSZYNSKI, JACK A. APPLICANT: GREENWALD, HOWARD J. APPLICANT: CURRY, STEPHEN H.
 PRIOR APPLICATION NUMBER: 10/867,517
PRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 418
 FILE REFERENCE: 1034312-000027
CURRENT APPLICATION NUMBER: US/11/063,439
CURRENT FILING DATE: 2005-02-23
 CURRENT APPLICATION NUMBER: US/11/063,439
CURRENT FILING DATE: 2005-02-23
 TITLE OF INVENTION: WATER-SOLUBLE COMPOUND FILE REFERENCE: 1034312-000027
 PRIOR APPLICATION NUMBER: 10/878,905 PRIOR FILING DATE: 2004-06-28
 PRIOR FILING DATE: 2004-03-24
 LENGTH: 3485
TYPE: PRT
 TYPE: PRT
ORGANISM: Zea mays
 LENGTH: 3485
 Local Similarity
nes 12; Conserv
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 PatentIn version 3.3
 PatentIn version 3.3
 TTTTTTTTTTS 1849
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 CURRY, STEPHEN
GOSS, KENDRICK
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100.0%; Pred. No.
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 DB 7; Length 3485; 0.026; hes 0; Indels
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RESULT 13 US-11-063-439-45 ; Sequence 45, Application US/11063439

Publication No. US20060147371A1 GENERAL INFORMATION:

APPLICANT: TUSZYNSKI, JACK A. APPLICANT: GREENWALD, HOWARD J.

GREENWALD, HOWARD CURRY, STEPHEN H. GOSS, KENDRICK

TITLE OF INVENTION: WATER-SOLUBLE COMPOUND FILE REFERENCE: 1034312-000027
CURRENT APPLICATION NUMBER: US/11/063,439
CURRENT FILING DATE: 2005-02-23
PRIOR APPLICATION NUMBER: 10/878,905
PRIOR FILING DATE: 2004-06-28
PRIOR FILING DATE: 2004-06-29
PRIOR APPLICATION NUMBER: 10/923,615
PRIOR APPLICATION NUMBER: 10/923,615
PRIOR APPLICATION NUMBER: 60/516,134
PRIOR FILING DATE: 2003-10-31

SEQ ID NO 45 LENGTH: 3486

PRIOR FILING DATE: 2004-06-14 NUMBER OF SEQ ID NOS: 418 SOFTWARE: PatentIn version 3.3

PRIOR APPLICATION NUMBER: 10/808,618 PRIOR FILING DATE: 2004-03-24

FILING DATE: 2004-03-24 APPLICATION NUMBER: 10/867,517

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; TYPE: PRT; ORGANISM: Zea mays US-11-063-439-56
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 ; TYPE: PRT ; ORGANISM: Eleusine indica US-11-063-439-45
 PRIOR APPLICATION NUMBER: 10/878,905
PRIOR FILING DATE: 2004-06-28
PRIOR PELICATION NUMBER: 10/923,615
PRIOR FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: 60/516,134
PRIOR APPLICATION NUMBER: 10/808,618
PRIOR APPLICATION NUMBER: 10/808,618
PRIOR APPLICATION NUMBER: 10/807,517
PRIOR FILING DATE: 2004-06-14
PRIOR FILING DATE: 2004-06-14
 Query Match
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Matches 12; Conservative
 SEQ ID NO 56
 Matches 12;
 Query Match
Best Local Similarity
 GENERAL INFORMATION:
 FILE REFERENCE: 1034312-000027
CURRENT APPLICATION NUMBER: US/11/063,439
CURRENT FILING DATE: 2005-02-23
 APPLICANT: TUSZYNSKI, JACK A.
APPLICANT: GREENWALD, HOWARD J.
APPLICANT: CURRY, STEPHEN H.
APPLICANT: GOSS, KENDRICK
 NUMBER OF SEQ ID NOS: 418
 TITLE OF INVENTION: WATER-SOLUBLE COMPOUND
 LENGTH: 3487
 1834 TITTTTTTTTT 1845
 393 TTTTTTTTTTTS 404
393 TTTTTTTTTTS 404
 PatentIn version 3.3
 Application US/11063439
 2.2%; Score 12; illarity 100.0%; Pred. No. Conservative 0; Mismatci
 2.2%; Score 12; DB 7;
100.0%; Pred. No. 0.026;
 0; Mismatches
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 DB 7; Length 3486; 0.026;
 0; Indels
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 Gaps
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 Query Match
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Matches 12; Conserve
 ; ORGANISM: Arabidopsis thaliana US-11-063-439-42
 TITLE OF INVENTION: WATER-SOLUBLE COMPOUND FILE REFERENCE: 1034312-000027
CURRENT APPLICATION NUMBER: US/11/063,439
CURRENT FILING DATE: 2005-02-23
PRIOR APPLICATION NUMBER: 10/878,905
PRIOR FILING DATE: 2004-06-28
PRIOR FILING DATE: 2004-06-28
PRIOR FILING DATE: 2004-08-20
PRIOR FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: 60/516,134
PRIOR APPLICATION NUMBER: 60/516,134
PRIOR APPLICATION NUMBER: 60/516,134
PRIOR APPLICATION NUMBER: 10/808,618
PRIOR APPLICATION NUMBER: 10/808,618
PRIOR APPLICATION NUMBER: 10/807,517
PRIOR FILING DATE: 2004-03-24
PRIOR FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 418
 RESULT 15
US-11-063-439-42
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 ; SEQ ID NO 42
; LENGTH: 3488
; TYPE: PRT
 Sequence 42, Application US/11063439 Publication No. US20060147371A1 GENERAL INFORMATION:
 APPLICANT: TUSZYNSKI, JACK A.
APPLICANT: GREENWALD, HOWARD J.
APPLICANT: CURRY, STEPHEN H.
APPLICANT: GOSS, KENDRICK
 SOFTWARE: PatentIn version 3.3
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1836 TTTTTTTTTTS 1847
1836 TTTTTTTTTTS 1847
 393 TITTTTTTTTTS 404
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 2.2%; Score 12;
100.0%; Pred. No.
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| 22. 923 2 OSANA DIEDI 22. 938 2 OSANI CREW 23. 938 2 OSANI CREW 24. 938 2 OSANI CREW 25. 1006 2 OSANI CREW 25. 1007 2 OSANI CREW 25. 1008 2 OSANI 25. 1008 2 OSANI CREW 25. 1008 2 OSANI 25. 1008 2 OSANI CREW 25. 1008 2 OSANI 25. 1008 2 OSANI 25. 1008 2 OSANI 25                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 12 2.2 860 2 054MY9 DICDI 12 2.2 863 2 054Q23 DICDI 12 2.2 865 2 054Q23 DICDI 12 2.2 865 2 054TS9 DICDI 12 2.2 872 2 0262TS7 9MYCE 12 2.2 873 2 055GF7 DICDI 12 2.2 873 2 055GF7 DICDI 12 2.2 903 2 055GFS DICDI 12 2.2 903 2 055GFS DICDI 12 2.2 906 2 054K91 DICDI 12 2.2 908 2 055GFS DICDI 12 055GFS DICDI 1 |
| 12 2.2 923 2 OS4MN9 DICDI 12 2.2 948 2 OSAMS DICDI 12 2.2 948 2 OSAMS DICDI 12 2.2 948 2 OSAMS DICDI 12 2.2 949 2 OSAMS DICDI 12 2.2 940 2 OSAMS DICDI 12 2.2 1026 1 GLT DROME 12 2.2 1026 2 OSAMS DICDI 12 2.2 1036 2 OSAMS DICDI 12 2.2 1037 2 OSAMS DICDI 12 2.2 1038 2 OSAMS DICDI 12 2.2 1039 2 OSCENT CRYHO 12 2.2 1039 2 OSAMS DICDI 12 2.2 1031 2 OSAMS DICDI 12 2.2 1032 2 OSAMS DICDI 12 2.2 1035 2 OSAMS DICDI 12 2.2 1036 2 OSAMS DICDI 12 2.2 1036 2 OSAMS DICDI 12 2.2 1037 2 OSAMS DICDI 12 2.2 1038 2 OSAMS DICDI 12 2.2 1039 2 OSAMS DICDI 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 12 2.2 860 2 Q54MY9 DICDI 12 2.2 863 2 Q54Q23 DICDI 12 2.2 865 2 Q54TS2 DICDI 12 2.2 872 2 Q26257 DICDI 12 2.2 872 2 Q26257 DICDI 12 2.2 873 2 Q55GF7 DICDI 12 2.2 873 2 Q55GF7 DICDI 12 2.2 873 2 Q55GF7 DICDI 12 2.2 873 2 Q55GF5 DICDI 12 2.2 903 2 Q55GE5 DICDI 12 2.2 903 2 Q55GE5 DICDI 12 2.2 904 2 Q54K91 DICDI 12 2.2 905 2 Q54K90 DICDI 12 2.2 906 2 Q54K90 DICDI 12 2.2 908 2 Q54K90 DICDI 12 2.2 913 2 Q5CING Q54TS1 Q55TS1 G5TSPCOSTO G55TS1 G5TS1 G5TSPCOSTO G55TS1 G5TS1 G5TS1 G5TS1 G5TS1 G5TS1 G5TS1 G5TS1 G5TS1 G5TS1  |

| 317<br>318<br>319<br>320<br>320<br>322<br>322                                                                                                                            | 300<br>300<br>300<br>300<br>300<br>300<br>300<br>310<br>311<br>311                                                                                                                                                                                                                                                                                                                                             | 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2                                                                                                                                                                                                                                                                                                                                   | 270<br>271<br>271<br>272<br>273<br>274<br>275<br>276<br>277<br>277<br>280<br>280<br>288                                                                                                                                                                                                                                                                                                        | 2000 1000 1000 1000 1000 1000 1000 1000                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
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| trypanosom trypanosom destriterm drosophila drosophila drosophila drosophila dictyostel trypanosom plasmodium                                                            | Qstuli ratcus norv Q54ma0 dictyosteli Q9nil4 plasmodium Q86jn9 dictyosteli Q95uy4 plasmodium Q95uy6 plasmodium Q95uy6 plasmodium Q962u5 plasmodium Q9ni03 plasmodium Q9ni03 plasmodium Q6r5f0 mus musculu Q9w3q9 drosophila Q61023 trypanosoma Q9ni21 plasmodium Q962u6 plasmodium Q962u6 plasmodium Q4qps0 drosophila Q4qms0 drosophila Q4qms0 drosophila Q4qms0 trypanosoma Q9twf2 trypanosoma               | 696666666666666666666666666666666666666                                                                                                                                                                                                                                                                                                                                 | Q86jh8 dictyosteli Q55ba7 dictyosteli Q54kp2 dictyosteli Q86if3 dictyosteli Q86if3 dictyosteli Q86ih12 dictyosteli Q8ih12 dictyosteli Q8ih12 dictyosteli Q5cy21 cryptcospori Q5cy21 cryptcospori Q5cy21 dictyosteli Q86ius dictyosteli Q551n7 dictyosteli Q54rq8 dictyosteli Q54rq8 dictyosteli Q54rq8 dictyosteli Q86b02 dictyosteli Q85c32 dictyosteli Q55q5d dictyosteli Q55q5d dictyosteli | 0556i3 dictyosteli Q86kl8 dictyosteli Q54dm4 dictyosteli Q54dm4 dictyosteli Q54l90 dictyosteli Q54l90 dictyosteli Q54l90 dictyosteli Q54g55 dictyosteli Q54g56 dictyosteli Q54g56 cryptospori Q54g56 cryptospori Q54m5 dictyosteli Q54m5 dictyosteli Q54m5 dictyosteli Q54m6 dictyosteli Q54m6 dictyosteli Q54ir2 dictyosteli Q54xt3 dictyosteli Q54xt3 dictyosteli Q54xt3 dictyosteli Q55ax2 dictyosteli Q66iv6 dictyosteli Q86iv6 dictyosteli Q86iv6 dictyosteli                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
| 389<br>390<br>392<br>393<br>395<br>396                                                                                                                                   | 375<br>375<br>376<br>377<br>379<br>380<br>382<br>382<br>388<br>388<br>388                                                                                                                                                                                                                                                                                                                                      | 359<br>359<br>360<br>362<br>363<br>364<br>369<br>370                                                                                                                                                                                                                                                                                                                    | 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6                                                                                                                                                                                                                                                                                                                                                          | 33333333333333333333333333333333333333                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
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| 222222222<br>0000000                                                                                                                                                     |                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                | 0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,0,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |
| 139<br>139<br>140<br>143<br>143<br>146                                                                                                                                   | 128<br>128<br>128<br>128<br>128<br>128<br>129<br>130<br>131<br>131<br>133<br>134                                                                                                                                                                                                                                                                                                                               | 123<br>123<br>123<br>123<br>123<br>125<br>125<br>125<br>126                                                                                                                                                                                                                                                                                                             | 115<br>116<br>116<br>118<br>119<br>119<br>120<br>121<br>122<br>122                                                                                                                                                                                                                                                                                                                             | 102<br>102<br>102<br>104<br>107<br>109<br>109<br>110<br>1110<br>1110<br>1111<br>1112                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
|                                                                                                                                                                          |                                                                                                                                                                                                                                                                                                                                                                                                                |                                                                                                                                                                                                                                                                                                                                                                         |                                                                                                                                                                                                                                                                                                                                                                                                | QZUG66 ASPOR 2 O61033 TRYCR 2 Q4DGR8 TRYCR 2 Q4CZZ1 TRYCR 2 O61050 |
| P90601 trypanosoma Q6waz8 trypanosoma Q962w5 trypanosoma Q962w5 trypanosoma Q3kyc8 chimpanzee Q15776 trypanosoma Q8it82 plasmodium Q3r033 xylella fas Q3rgk9 xylella fas | Acribo trypanosoma Q4crbo trypanosoma Q4crbo trypanosoma Q4cuv2 trypanosoma Q4cuv2 trypanosoma Q4db74 trypanosoma Q4db74 trypanosoma Q4db74 trypanosoma Q4db74 trypanosoma Q4db74 trypanosoma Q4dc48 trypanosoma Q4db74 trypanosoma Q4db74 trypanosoma Q8db70 dictyosteli Q61037 trypanosoma | P90602 trypanosoma P90602 trypanosoma Q4cuv5 trypanosoma Q4dc51 trypanosoma Q4dc51 trypanosoma Q50900 plasmodium Q5n763 oryza sativ Q61025 trypanosoma Q4cly1 trypanosoma Q4cly1 trypanosoma Q4ch75 trypanosoma Q4ch75 trypanosoma Q4ch52 trypanosoma Q4ch52 trypanosoma Q5962w4 trypanosoma Q5962 candida alb Q61021 trypanosoma Q61056 trypanosoma Q4db73 trypanosoma |                                                                                                                                                                                                                                                                                                                                                                                                | Q2ug66 aspergillus 061033 trypanosoma Q4dgr8 trypanosoma Q4dgr8 trypanosoma Q4dz21 trypanosoma Q2vk93 drosophila Q4cz21 trypanosoma 061050 trypanosoma 061050 trypanosoma Q91619 pneumocysti Q6pn90 plasmodium Q5a4h8 candida alb Q9ni17 plasmodium Q9ni16 plasmodium Q9ni17 plasmodium Q9ni18 plasmodium Q9ni18 plasmodium Q9ni26 plasmodium Q9ni26 plasmodium Q9ni26 plasmodium Q5zdk7 oryza sativ Q9bjn8 plasmodium                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |

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| 105<br>1173<br>1173<br>1174<br>1174<br>1174<br>1175<br>1177<br>1177<br>1177<br>1180<br>1181<br>1181<br>1183<br>1183<br>1183<br>1183<br>1183                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 146<br>147<br>148<br>148<br>148<br>148<br>150<br>150<br>150<br>150<br>150<br>152<br>152<br>153<br>155<br>155<br>155<br>155<br>157<br>166                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
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| Q4e3dl trypanosoma Q4e428 trypanosoma Q4d496 trypanosoma Q4d4616 trypanosoma Q4d4616 trypanosoma Q4d4616 trypanosoma Q4d418 trypanosoma Q4d418 trypanosoma Q4d418 trypanosoma Q4d418 trypanosoma Q4d418 trypanosoma Q4d400 trypanosoma Q4d401 trypanosoma Q4d411 trypanosoma Q4d411 trypanosoma Q4d411 trypanosoma Q4c211 trypanosoma Q4c011 trypanosoma Q4c012 trypanosoma Q4c012 trypanosoma Q4c014 trypanosoma Q4c014 trypanosoma Q4c015 trypanosoma Q4c015 trypanosoma Q4c015 trypanosoma Q4c015 trypanosoma Q4c016 trypanosoma Q4c017 trypanosoma Q4c018 trypanosoma Q4c019 trypanosoma Q4c011 trypanosoma Q4c011 trypanosoma Q4c011 trypanosoma Q4c012 trypanosoma Q4c013 eptatretus Q4g113 eptatretus Q4g114 trypanosoma Q4c014 trypanosoma Q4c015 trypanosoma Q4c016 trypanosoma Q4d06 trypanosoma Q4d06 trypanosoma Q4d07 trypanosoma Q4d08 trypanosoma Q4d08 trypanosoma Q4d11 eptatretus Q4g111 Q9u26 caenorhabdi Q5d423 caenorhabdi Q5d423 caenorhabdi Q5d421 ceptatretus Q4g114 eptatretus Q4g116 eptatretus                                                                                                                                                                                                                                                             |                                       |
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MEDLINE=98339885; PubMed=9673266;
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PubMed=16272509; DOI=10.1128/JCM.43.11.5715-5720.2005;
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GO; GO:0004872; F:receptor activity; IF GO; GO:0007155; P:cell adhesion; IEA. InterPro; IPR003536; Tir receptor. IPR03536; Tir receptor. IPR03549; NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=0157:H7 / Sakai / RIMD 0509952 / EHEC;

MEDLINE=21156231; PubMed=11258796; DOI=10.1093/dnares/8.1.11;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli
0157:H7 and genomic comparison with a laboratory strain K-12.";
 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=0157:H7 / EDL933 / ATCC 700927 / EBLE7

MEDLINE=21074935; pubmed=11206551; DOI=10.1038/35054089;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kipatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

"Genome sequence of enterobaemorrhagic Escherichia coli 0157:H7."

Nature 409:529-533(2001).
 Complete proteome; Receptor. SEQUENCE 558 AA; 58022 MW;
 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
 DNA Res. 8:11-22(2001).
 Enterobacteriaceae; Escherichia.
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 OB5506;
OB5506;
01-NOV-1998,
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SEQUENCE
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PRINTS; PR01370; TRNSINTIMINR.
 Paton A.W., Manning P.A., Woodrow M.C., Paton J.C.; "Translocated intimin receptors (Tir) of Shiga-toxigenic coli isolates belonging to serogroups 026, 0111, and 0157 sera from patients with hemolytic-uremic syndrome and exh
 GO; GO:0004872; F:receptor activ
GO; GO:0007155; P:cell adhesion;
 EMBL; AF070067; AAC69314.1; -; HSSP; Q9KWH9; 1F02.
 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
 sequence heterogeneity.";
Infect. Immun. 66:5580-5586(1998).
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STRAIN=CPG122-G57, and CPG6;
PubMed=16272509; DOI=10.1128/JCM.43.11.5715-5720.2005;
PubMed=16272509; DOI=10.1128/JCM.43.11.5715-5720.2005;
Garmendia J., Ren Z., Tennant S., Midolli Viera M.A., Chon Whale A., Azzopardi K., Dahan S., Sircili M.P., Franzolin Trabulsi L.R., Phillips A., Gomes T.A., Xu J., Robins-Brow
 Pfam; PF07489; Tir_receptor_C; Pfam; PF03549; Tir_receptor_M; Pfam; PF07490; Tir_receptor_N Pfam; PF07490; TRNSINTIMINR.
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 EMBL; DQ007020; AAY25391.1; -; EMBL; DQ007019; AAY25390.1; -;
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 "Distribution of tccP in Clinical Enterohemorrhagic
Enteropathogenic Escherichia coli Isolates.";
J. Clin. Microbiol. 43:5715-5720(2005).
 Frankel G.;
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 Enterobacteriaceae;
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26-APR-2005,
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PRINTS; PR01370; TRNSINTIMINR.
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 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Hohn C., Karns J.S., Higgins J.A.;
Submitted (FEB-2005) to the EMBL/GenBank/DDBJ databases
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PubMed=15870341; DOI=10.1128/AEM.71.5.2511-2519.2005;
Higgins J.A., Belt K.T., Karns J.S., Russell-Anelli J., S
"tir- and stx-Positive Escherichia coli in Stream Waters
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 AY944737; AAX47730.1; -; Genomic_DNA.
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RESULT 6
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STRAIN=CDC 1843-73T, and DBS100;

MEDLINE=2055330; PubMed=11101562;

Luperchio S.A., Newman J.V., Dangler C.A., Schrenzel M.D.,

Brenner D.J., Steigerwalt A.G., Schauer D.B.;

"Citrobacter rodentium, the causative agent of transmissible murine colonic hyperplasia, exhibits clonality: synonymy of C. rodentium an mouse-pathogenic Escherichia coli.";

J. Clin. Microbiol. 38:4343-4350(2000).
 EMBL;
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OPETII;
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O1-MAR-2001, sequence version 1.
O7-FEB-2006 entry version 12.
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SEQUENCE
 MEDLINE=21437640; PubMed=11553577;
DOI=10.1128/IAI.69.10.6323-6335.2001;
Deng W., Li Y., Vallance B.A., Finlay B.B.;
"Locus of enterocyte effacement from Citrobacter rodentium:
analysis and evidence for horizontal transfer among attachir
 O7BHL5;
O5-JUL-2004, integrated into UniProtKB/TrEMBL.
O5-JUL-2004, sequence version 1.
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 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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GO; GO:0007155; F:cell adhesion; II
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 Okutani A., Itoh K., Sasakawa C.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
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Paton A.W., Manning P.A., Woodrow M.C., Paton J.C.;
Paton A.W., Manning P.A., Woodrow M.C., Paton J.C.;
"Translocated intimin receptors (Tir) of Shiga-toxigenic Escherichia coli isolates belonging to serogroups 026, Oll1, and Ol57 react with sera from patients with hemolytic-uremic syndrome and exhibit marked
 Paton A.W., Manning P.A., Woodrow M.C., Paton J.C.;
"Translocated intimin receptors (Tir) of Shiga-toxigenic Escherichia
coli isolates belonging to serogroups O26, O111, and O157 react with
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STRAIN=REPEC 84/110/1,
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 Marches O., Nougayrede J.-P., Boullier S., Mainil J., Charlier G., Raymond I., Pohl P., Boury M., De Rycke J., Milon A., Oswald E.; "Role of tir and intimin in the virulence of rabbit enteropathogenic Escherichia coli serotype O103.H2."; Infect. Immun. 68:2171-2182(2000).
 EMBL;
 Deibel C., Kraemer S., Chakraborty T., Ebel F.; "EspE, a novel secreted protein of attaching and effacing bacteria, directly translocated into infected host cells where it appears as tyrosine-phosphorylated 90 kDa protein."; Mol. Microbiol. 28:463-474(1998).
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 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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 Tauschek M., Strugnell R.A., Robins-Browne R.M.; "Characterization and evidence of mobilization of the "Characterization and eridence of mobilization of engathogenicity island of rabbit-specific strains of engathogenicity
 MEDLINE=97055784; PubMed=8900070; DOI=10.1016/0378-1097(96)00371-0; Agin T.S., Cantey J.R., Boedeker E.C., Wolf M.K.; "Characterization of the eaeA gene from rabbit enteropathogenic Escherichia coli strain RDEC-1 and comparison to other eaeA genes f bacteria that cause attaching-effacing lesions."; FEMS Microbiol. Lett. 144:249-258(1996).
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MEDLINE=97055784; PubMed=8900070;
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Elliott S.J., Walnwright L.A., McDaniel T.K., Jarvis K.G., De
Lai L.C., McNamara B.P., Donnenberg M.S., Kaper J.B.;
"The complete sequence of the locus of enterocyte effacement
from enteropathogenic Escherichia coli E2348/69.";
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 Mol. Microbiol. 44:1533-1550(2002).
 MEDLINE=21153569; PubMed=11254564;
DOI=10.1128/IAI.69.4.2107-2115.2001;
Zhu C., Agin T.S., Elliott S.J., Johnson L.A., Thate T.E.,
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STRAIN=RDEC-1;
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 Agin T.S., Boedeker E.C.
Submitted (JAN-1998) to
 Escherichia coli."
 "Complete nucleotide sequence and analysis of the locus of enterocyte sffacement from rabbit diarrheagenic Escherichia coli RDEC-1."; infect. Immun. 69:2107-2115(2001).
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 Jores J., Wagner S.K., Rumer L., Eichberg J., Laturr Schierack P., Tschaepe H., Wieler L.H.; "Description of a 111-kb pathogenicity island (PAI) virulence features in the enterohemorrhagic E. coli RW1374 (0103:H2) and detection of a similar PAI in c
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 Jores J., Rumer L., Kiessling S., Kaper J.B., Wieler L.H.;
"Identification of a new pathogenicity island inserted in the pheV
tRNA gene of the bovine Shiga toxin-producing E. coli strain RW1374
(0103:H2) harboring a locus of entercyte effacement that is flanked
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Int. J. Med. Microbiol. 294:417-425(2005).
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